

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:12:01 ; Search time 118.268 Seconds
(without alignments)
755.417 Million cell updates/sec

Title: US-09-807-990A-124

Perfect score: 1190
Sequence: 1 LALVATGNDTTRTPDLYLYK.....PAFQQQLCKAKAFHQHKK 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1190	100.0	249	2	AAW06463 Escherich
2	1190	100.0	249	2	AAW71029 Acid phos
3	1190	100.0	249	4	AAW75064 Escherich
4	1183	99.4	231	2	AAW71034 Mutant ac
5	1178	99.0	231	2	AAW71035 Mutant ac
6	1161	97.6	231	2	AAW71036 Mutant ac
7	1155	97.1	231	2	AAW71037 Mutant ac
8	1152	96.8	231	2	AAW71038 Mutant ac
9	1141	95.9	231	2	AAW71039 Mutant ac
10	1137	95.5	231	2	AAW71040 Mutant ac
11	1133	95.2	231	2	AAW71041 Mutant ac
12	1129	94.9	231	2	AAW71042 Mutant ac
13	1096	92.1	253	7	ABO61416 Klebsiell
14	1095	92.0	248	2	AAW06458 Enterobac
15	1095	92.0	248	2	AAW71031 Acid phos
16	1080	90.8	248	2	AAW06459 Klebsiell
17	1080	90.8	248	4	AAW71032 Acid phos
18	1049	88.2	248	4	AAW75068 Enterobac
19	986	82.9	248	2	AAW06457 Providenc
20	986	82.9	248	2	AAW71030 Acid phos
21	969	81.4	249	2	AAW06462 Morganell
22	969	81.4	249	4	AAW71028 Acid phos
23	969	81.4	249	4	AAW75065 Morganell
24	965	81.1	249	4	AAU27583 Fusion pr
25	768	64.5	244	2	AAW06460 Serratia

26	768	64.5	244	2	AAW71033 Acid phos
27	577	48.5	246	2	AAW54082 Virulence
28	572	48.1	246	2	AAW35759 Adyrase (
29	480	40.3	232	4	AAW75066 Salmonell
30	329	27.6	264	4	AAW75067 Zymomonas
31	312	26.2	252	2	AAW20014 Ascorbic
32	191	16.1	428	7	ABO64424 Klebsiell
33:	181	15.2	943	8	ADL05772 M. catarr
34	176.5	14.8	585	8	ADG32050 Mutant B_
35	176.5	14.8	594	8	ADG32068 Mutant B_
36	173.5	14.6	253	7	ABO79811 Pseudomon
37	149.5	12.6	508	4	AAU56365 Propionib
38	149.5	12.6	508	6	ABM52884 Bacterial
39	147	12.4	987	7	ADF07500 Bacteri
40	143	12.0	622	4	AAW91063 C glutami
41	143	12.0	622	7	ADJ87369 DNA repli
42	129.5	10.9	513	5	ABP65275 Bifidobac
43	106.5	8.9	201	7	ADM26585 Hyperther
44	105	8.8	58	5	ABP08795 Human ORF
45	99.5	8.4	353	8	ADL43241 Plant tra

ALIGNMENTS

RESULT 1
ID AAW06463 standard; protein, 249 AA.
XX
AC AAW06463;
XX
DT 13-AUG-1997 (first entry)
XX
DE Escherichia blattae JCM 1650 acid phosphatase.
XX
KM JCM 1650; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
XX condition; pharmaceutical; intermediate.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= sig_peptide
FT Peptide 19..249
FT /label= mat_peptide
FT Misc-difference 92
FT /note= "optionally replaced by another amino acid"
FT Misc-difference 171
FT /note= "optionally replaced by another amino acid"
XX
PN W09637603-A1.
XX
PD 28-NOV-1996.
XX
PF 24-MAY-1996; 96WO-JP001402.
XX
PR 25-MAY-1995; 95UP-00149781.
XX 26-MAR-1996; 96UP-00094680.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
PI Mihara Y, Uragawa T, Yamada H, Asano Y;
XX WPI; 1997-021215/02.
XX
DR N-PSDB; AAT45011.
XX
XX Efficient production of nucleoside 5'-phosphate - by reaction of a
XX nucleoside with a phosphoric acid donor in the presence of an acid
XX phosphatase.
XX
PS Claim 3; Page 56-58; 95pp; Japanese.
XX
XX The present sequence is the Escherichia blattae JCM 1650 acid phosphatase

(AP), which can be used to produce a nucleoside 5'-phosphate ester from the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl-, or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5. The PA can be used for the economic and efficient production of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and intermediates for pharmaceuticals

Sequence 249 AA:

Query Match 100.0%; Score 1190; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTPKPDLYLKNSEAINSLALPPPPAVGSAFLNDQMYEGRLNTER 60
DB 19 LALVATGNDTTPKPDLYLKNSEAINSLALPPPPAVGSAFLNDQMYEGRLNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 138
QY 121 IRPPAFYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELNFORQNEILKRGYELG 180
DB 139 IRPPAFYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELNFORQNEILKRGYELG 198
QY 181 QSRVIGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 231
DB 199 QSRVIGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 249

RESULT 2

AAW71029 standard; protein; 249 AA.

AAW71029;
21-OCT-1998 (first entry)
Acid phosphatase enzyme amino acid sequence.
Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning; intermediate.
Escherichia blattae.
Key Location/Qualifiers
FT 1..18
FT /note= "signal peptide"
FT 19..249
FT /note= "mature protein; Claim 6"

EP857788-A2.

12-AUG-1998.

20-NOV-1997; 97EP-00309365.

21-NOV-1996; 96JP-00311103.

18-JUN-1997; 97JP-00161674.

(AJIN) AJINOMOTO CO INC.

Mihara Y, Utagawa T, Yamada H, Asano Y;

WPI; 1998-416010/36.

N-PSDB; AAIV43046.

Preparation of nucleoside 5'-phosphates comprises reacting nucleoside with phosphate donor in presence of acid phosphatase - used as seasonings or pharmaceutical intermediates.

Example 12; Page 35-36; 83pp; English.

CC The present sequence represents an acid phosphatase enzyme. The
CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate esters. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them

Sequence 249 AA:

Query Match 100.0%; Score 1190; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTPKPDLYLKNSEAINSLALPPPPAVGSAFLNDQMYEGRLNTER 60
DB 19 LALVATGNDTTPKPDLYLKNSEAINSLALPPPPAVGSAFLNDQMYEGRLNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKDHMR 138
QY 121 IRPPAFYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELNFORQNEILKRGYELG 180
DB 139 IRPPAFYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELNFORQNEILKRGYELG 198
QY 181 QSRVIGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 231
DB 199 QSRVIGYHMQSDVDARVVGSAVVATLHTNPAFQOOLQAKAEFAHQHKK 249

RESULT 3

AAW75064 standard; protein; 249 AA.

AAW75064;
23-JUN-2001 (first entry)
Escherichia blattae nucleoside-5'-phosphate producing enzyme protein.
Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
transphosphorylation; phosphatase; protein co-ordinate data;
X-ray structural analysis; three-dimensional structure.

Escherichia blattae.

WO200118184-A1.

15-MAR-2001.

01-SEP-2000; 2000WO-IP005973.

03-SEP-1999; 99JP-00249545.

(AJIN) AJINOMOTO CO INC.

Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;

Kuratsashi O, Konda T, Shimaoka M, Kozutsumi R, Asano Y;

WPI; 2001-380914/40.

N-PSDB; AAH19701.

Variant enzyme having elevated nucleoside 5'-prime phosphate producing activity and having a specific three-dimensional structure for production of nucleotides as pharmaceutical intermediates.

Disclosure; Page 107; 150pp; Japanese.

The present invention describes a variant nucleoside-5'-phosphate producing enzyme which is a modification of a transphosphorylase or

CC phosphatase which contains a lysine, two arginine and two histidine
CC residues and in which the C-alpha distances between these residues are
CC enclosing a space which permits the binding of a nucleoside with these
CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
CC expression vectors containing the DNA; (3) host cells transformed by the
CC vectors; (4) preparation of the variant enzyme by culture of the
CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
CC with methylbenzidic acid; and (6) selection of inhibitors of acid phosphatase
CC or transphosphorylase using the structural coordinates derived from the
CC enzyme. The variant enzymes with increased efficiency for production of
CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
CC AAH19701 to AAH19785 and AAB75064 to AAB75101 represent sequences used in
CC the exemplification of the present invention

SQ Sequence 249 AA;

Query Match 100.0%; Score 1190; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.2e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLVYLNKSEAINSLALPPPPAVGSIAPLNDQAMYEGRLLRNER 60
DB 19 LALVATGNDTTTKPDLVYLNKSEAINSLALPPPPAVGSIAPLNDQAMYEGRLLRNER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 120
DB 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 138
QY 121 IRPFAFGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPOREILKRGYELG 180
DB 139 IRPFAFGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPOREILKRGYELG 198
QY 181 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAHQKK 231
DB 199 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAHQKK 249

RESULT 4

AAW71034
ID AAW71034 standard; protein; 231 AA.

AAW71034;

DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blatae.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
mutant; intermediate.OS Synthetic.
OS Escherichia blatae.FH Key Location/Qualifiers
FT Misc-difference 74
FT /label= G74D

EP857788-A2.

PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.

PR 21-NOV-1996; 96JP-00311103.

PR 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utegawa T, Yamada H, Asano Y;

PR WPI, 1998-416010/36.

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside

PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.

PS Example 19; Page; 83pp; English.

CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided

SQ Sequence 231 AA;

Query Match 99.4%; Score 1183; DB 2; Length 231;
Best Local Similarity 99.6%; Pred. No. 2.6e-118;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLVYLNKSEAINSLALPPPPAVGSIAPLNDQAMYEGRLLRNER 60
DB 1 LALVATGNDTTTKPDLVYLNKSEAINSLALPPPPAVGSIAPLNDQAMYEGRLLRNER 60
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 120
DB 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGLATRSADHYMR 120
QY 121 IRPFAFGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPOREILKRGYELG 180
DB 121 IRPFAFGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPOREILKRGYELG 180
QY 181 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAHQKK 231
DB 181 OSRVICGYHMOSDVAARVGSAAVATLTHTNPAFQOOLQKAKAEPAHQKK 231

RESULT 5

AAW71035
ID AAW71035 standard; protein; 231 AA.

AAW71035;

DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blatae.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
mutant; intermediate.OS Synthetic.
OS Escherichia blatae.FH Key Location/Qualifiers
FT Misc-difference 74
FT /label= G74D
FT Misc-difference 153
FT /label= 1153T

EP857788-A2.

PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.

PR 21-NOV-1996; 96JP-00311103.

PR 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

```

XX MIhara Y, Utogawa T, Yamada H, Asano Y;
PI WPI; 1998-416010/36.
DR
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them, note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
SQ Sequence 231 AA;
Query Match 99.0%; Score 1178; DB 2; Length 231;
Best Local Similarity 99.1%; Pred. No. 9.1e-118;
Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMYEQGRLLNTER 60
DB 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMYEQGRLLNTER 60
QY 61 GKLAEDANLSSGCVANAFSGAFSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 120
DB 61 GKLAEDANLSSGCVANAFSGAFSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 120
QY 121 IRPFAFYGVSTCNTTTEODKLSKNGSPSGHTSIGMTALVLAINEPQRONEILKGYELG 180
DB 121 IRPFAFYGVSTCNTTTEODKLSKNGSPSGHTSIGMTALVLAINEPQRONEILKGYELG 180
QY 181 QSRVICGYHMOGSDVDAARVGSAVVAATLTNPAPFOOQOKAKAEFAOHOKK 231
DB 181 QSRVICGYHMOGSDVDAARVGSAVVAATLTNPAPFOOQOKAKAEFAOHOKK 231

RESULT 6
AAW71036
ID AAW71036 standard; protein; 231 AA.
XX
XX AAW71036;
AC
XX 21-OCT-1998 (first entry)
DT
XX
XX Mutant acid phosphatase enzyme of Escherichia blattae.
DE
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
XX Synthetic.
OS Escherichia blattae.
XX
XX Key Location/Qualifiers
FH Misc-difference 63
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66
FT Misc-difference 66 /label= E66A
FT Misc-difference 74
FT Misc-difference 74 /label= G74D
FT Misc-difference 153

```

```

FT /label= I153T
XX
XX EP857788-A2.
PN
XX
XX 12-AUG-1998.
PD
XX
XX 20-NOV-1997; 97BP-00309365.
PF
XX
XX 21-NOV-1996; 96JP-00311103.
PR
XX
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX MIhara Y, Utogawa T, Yamada H, Asano Y;
PI WPI; 1998-416010/36.
DR
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them, note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
SQ Sequence 231 AA;
Query Match 97.6%; Score 1161; DB 2; Length 231;
Best Local Similarity 97.8%; Pred. No. 6.1e-116;
Matches 226; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMYEQGRLLNTER 60
DB 1 LALVATGNDTTTTPDLYYLKNSSEAINSLALPPPPVAGSIAFLNDQAMYEQGRLLNTER 60
QY 61 GKLAEDANLSSGCVANAFSGAFSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 120
DB 61 GKLAEDANLSSGCVANAFSGAFSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 120
QY 121 IRPFAFYGVSTCNTTTEODKLSKNGSPSGHTSIGMTALVLAINEPQRONEILKGYELG 180
DB 121 IRPFAFYGVSTCNTTTEODKLSKNGSPSGHTSIGMTALVLAINEPQRONEILKGYELG 180
QY 181 QSRVICGYHMOGSDVDAARVGSAVVAATLTNPAPFOOQOKAKAEFAOHOKK 231
DB 181 QSRVICGYHMOGSDVDAARVGSAVVAATLTNPAPFOOQOKAKAEFAOHOKK 231

RESULT 7
AAW71037
ID AAW71037 standard; protein; 231 AA.
XX
XX AAW71037;
AC
XX
XX 21-OCT-1998 (first entry)
DT
XX
XX Mutant acid phosphatase enzyme of Escherichia blattae.
DE
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
XX Synthetic.
OS

```


OS Escherichia blattae.

XX Key Location/Qualifiers

FT Misc-difference 63

FT Misc-difference /label= L63Q

FT Misc-difference 65

FT Misc-difference /label= A65Q

FT Misc-difference 66

FT Misc-difference /label= B66A

FT Misc-difference 74

FT Misc-difference /label= G74D

FT Misc-difference 85

FT Misc-difference /label= S85Y

FT Misc-difference 153

FT Misc-difference /label= I153T

XX

XX EP857788-A2.

XX PD 12-AUG-1998.

XX PF 20-NOV-1997; 97BP-00309365.

XX PR 21-NOV-1996; 96JP-00311103.

XX PR 18-JUN-1997; 97JP-00161674.

XX PA (AJIN) AJINOMOTO CO INC.

XX PI Minara Y, Utagawa T, Yamada H, Asano Y;

XX DR WPI, 1998-416010/36.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

RESULT 8

AAW71038

XX ID AAW71038 standard; protein; 231 AA.

XX AC AAW71038;

XX DT 21-OCT-1998 (first entry)

XX DE Mutant acid phosphatase enzyme of Escherichia blattae.

XX KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

XX KM mutant; intermediate.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

AAW71038

XX ID AAW71038 standard; protein; 231 AA.

XX AC AAW71038;

XX DT 21-OCT-1998 (first entry)

XX DE Mutant acid phosphatase enzyme of Escherichia blattae.

XX KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

XX KM mutant; intermediate.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

AAW71038

XX ID AAW71038 standard; protein; 231 AA.

XX AC AAW71038;

XX DT 21-OCT-1998 (first entry)

XX DE Mutant acid phosphatase enzyme of Escherichia blattae.

XX KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

XX KM mutant; intermediate.

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

```

Db      1 LALVATGNDTTTKDLYLYLNKSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTER 60
Qy      61 GKLAEDANLSSGGVANAFCGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKOHYMR 120
Db      61 GKQAQADADLAAGVANAFCGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKOHYMR 120
Qy      121 IRPPAFYGVSTCNTKODDKLSKNGSYSGHTSGMTATLVLAETNPORONEILKRGYEIG 180
Db      121 IRPPAFYGVSTCNTKODDKLSKNGSYSGHTSGMTATLVLAETNPORONEILKRGYEIG 180
Qy      181 QSRVTCGYHMQSDVDARVVGSAVAVATLTHTNPAFQOOLQAKAEFAQHOKK 231
Db      181 QSRVTCGYHMQSDVDARVVGSAVAVATLTHTNPAFQOOLQAKAEFAQHOKK 231

```

RESULT 9

AAW71039
ID AAW71039 standard; protein; 231 AA.

AC AAW71039;

DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blattae.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning; mutant; intermediate.

OS Synthetic.

OS Escherichia blattae.

FX Key Location/Qualifiers

```

FT MISC-difference 63 /label= L63Q
FT MISC-difference 65 /label= A65Q
FT MISC-difference 66 /label= E66A
FT MISC-difference 69 /label= N69D
FT MISC-difference 71 /label= S71A
FT MISC-difference 72 /label= S72A
FT MISC-difference 74 /label= G74D
FT MISC-difference 135 /label= T135K
FT MISC-difference 136 /label= E136D
FT MISC-difference 153 /label= I153T

```

EN EP857788-A2.

PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.

PR 21-NOV-1996; 96JP-00311103.

PR 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utogawa T, Yamada H, Amano Y;

DR WPI; 1998-416010/36.

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside with phosphate donor in presence of acid phosphatase - used as seasonings or pharmaceutical intermediates.

PS Example 19; Page; 83pp; English.

CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were created using the mature protein of AAW71029. The specification describes a method for the preparation of nucleoside 5'-phosphate esters. The method comprises reacting a nucleoside with a phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that has been altered to increase its affinity for the nucleoside and/or to increase its thermal stability, or in the presence of a microorganism that has been transformed with recombinant DNA containing a gene coding for such an acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or pharmaceuticals or as intermediates for them. note: this sequence does not appear in the specification; it was created using information provided

CC Sequence 231 AA;

Query Match 95.9%; Score 1141; DB 2; Length 231;

Best Local Similarity 95.7%; Pred. No. 8.6e-114;

Matches 221; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

Qy      1 LALVATGNDTTTKDLYLYLNKSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTER 60
Db      1 LALVATGNDTTTKDLYLYLNKSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTER 60
Qy      61 GKLAEDANLSSGGVANAFCGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKOHYMR 120
Db      61 GKQAQADADLAAGVANAFCGAFSPITTEKDAAPALHKLNTNMIEDAGDLATRSKOHYMR 120
Qy      121 IRPPAFYGVSTCNTKODDKLSKNGSYSGHTSGMTATLVLAETNPORONEILKRGYEIG 180
Db      121 IRPPAFYGVSTCNTKODDKLSKNGSYSGHTSGMTATLVLAETNPORONEILKRGYEIG 180
Qy      181 QSRVTCGYHMQSDVDARVVGSAVAVATLTHTNPAFQOOLQAKAEFAQHOKK 231
Db      181 QSRVTCGYHMQSDVDARVVGSAVAVATLTHTNPAFQOOLQAKAEFAQHOKK 231

```

RESULT 10

AAW71040
ID AAW71040 standard; protein; 231 AA.

AC AAW71040;

DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blattae.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning; mutant; intermediate.

OS Synthetic.

OS Escherichia blattae.

FX Key Location/Qualifiers

```

FT MISC-difference 63 /label= L63Q
FT MISC-difference 65 /label= A65Q
FT MISC-difference 66 /label= E66A
FT MISC-difference 69 /label= N69D
FT MISC-difference 71 /label= S71A
FT MISC-difference 72 /label= S72A
FT MISC-difference 74 /label= G74D
FT MISC-difference 116 /label= D116E
FT MISC-difference 135 /label= T135K

```

```

FT  Misc-difference 136
FT  /label= E136D
FT  Misc-difference 153
FT  /label= I153T
XX
XX  EP857788-A2.
XX  12-AUG-1998.
XX
XX  20-NOV-1997; 97EP-00309365.
XX
XX  21-NOV-1996; 96JP-00311103.
XX  18-JUN-1997; 97JP-00161674.
XX
XX  (AJIN ) AJINOMOTO CO INC.
XX
XX  Mihara Y, Utogawa T, Yamada H, Asano Y;
XX
XX  WPI; 1998-416010/36.
XX
XX  Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX  with phosphate donor in presence of acid phosphatase - used as seasonings
XX  or pharmaceutical intermediates.
XX
XX  Example 19; Page; 83pp; English.
XX
XX  AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX  created using the mature protein of AAW71029. The specification describes
XX  a method for the preparation of nucleoside 5'-phosphate esters. The
XX  method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX  5.5 in the presence of an acid phosphatase that has been altered to
XX  increase its affinity for the nucleoside and/or to increase its thermal
XX  stability, or in the presence of a microorganism that has been
XX  transformed with recombinant DNA containing a gene coding for such an
XX  acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX  pharmaceuticals or as intermediates for them. note: this sequence does
XX  not appear in the specification; it was created using information
XX  provided
XX
XX  Sequence 231 AA;
SQ
Query Match 95.5%; Score 1137; DB 2; Length 231;
Best Local Similarity 95.2%; Pred. No. 2,3e-113;
Matches 220; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKDLYLYLKNSEAINSLALPPPPAVGSIAFNDQAMYEGRLLRNTER 60
DB 1 LALVATGNDTTTKDLYLYLKNSEAINSLALPPPPAVGSIAFNDQAMYEGRLLRNTER 60
QY 61 GKLAEDANLSSGCVANAFSGAFSGPITEKAPALHKLTTWTEPAGDLATRSADHYMR 120
DB 61 GKQAQADADLAAGDVANAFSGAFSGPITEKAPALHKLTTWTEPAGDLATRSADHYMR 120
QY 121 IRPFAFYGVSTCNTTEODPKLSKNGSPSGHTSIGWATLVLAEINPQRONEILKRGYELG 180
DB 121 IRPFAFYGVSTCNTTEODPKLSKNGSPSGHTSIGWATLVLAEINPQRONEILKRGYELG 180
QY 181 QSRVYICGYHWOSDVDAARVGSAAVVATLHTNPAFOQOLQKAKAEFAQHOKK 231
DB 181 QSRVYICGYHWOSDVDAARVGSAAVVATLHTNPAFOQOLQKAKAEFAQHOKK 231

RESULT 11
AAW71041
ID AAW71041 standard; protein; 231 AA.
XX
XX  AAW71041;
XX
XX  21-OCT-1998 (first entry)
XX
XX  Mutant acid phosphatase enzyme of Escherichia blactae.
XX
XX  Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

```

```

KW mutant; intermediate.
XX
XX  Synthetic.
OS  Escherichia blactae.
XX
XX  Key Location/Qualifiers
XX  FH Misc-difference 63
XX  FT /label= L63Q
XX  FT Misc-difference 65
XX  FT /label= A65Q
XX  FT Misc-difference 66
XX  FT /label= B66A
XX  FT Misc-difference 69
XX  FT /label= N69D
XX  FT Misc-difference 71
XX  FT /label= S71A
XX  FT Misc-difference 72
XX  FT /label= S72A
XX  FT Misc-difference 74
XX  FT /label= G74D
XX  FT Misc-difference 116
XX  FT /label= D116E
XX  FT Misc-difference 130
XX  FT /label= S130E
XX  FT Misc-difference 135
XX  FT /label= T135K
XX  FT Misc-difference 136
XX  FT /label= E136D
XX  FT Misc-difference 153
XX  FT /label= I153T
XX
XX  EP857788-A2.
XX
XX  12-AUG-1998.
XX
XX  20-NOV-1997; 97EP-00309365.
XX
XX  21-NOV-1996; 96JP-00311103.
XX  18-JUN-1997; 97JP-00161674.
XX
XX  (AJIN ) AJINOMOTO CO INC.
XX
XX  Mihara Y, Utogawa T, Yamada H, Asano Y;
XX
XX  WPI; 1998-416010/36.
XX
XX  Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX  with phosphate donor in presence of acid phosphatase - used as seasonings
XX  or pharmaceutical intermediates.
XX
XX  Example 19; Page; 83pp; English.
XX
XX  AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX  created using the mature protein of AAW71029. The specification describes
XX  a method for the preparation of nucleoside 5'-phosphate esters. The
XX  method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX  5.5 in the presence of an acid phosphatase that has been altered to
XX  increase its affinity for the nucleoside and/or to increase its thermal
XX  stability, or in the presence of a microorganism that has been
XX  transformed with recombinant DNA containing a gene coding for such an
XX  acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX  pharmaceuticals or as intermediates for them. note: this sequence does
XX  not appear in the specification; it was created using information
XX  provided
XX
XX  Sequence 231 AA;
SQ
Query Match 95.2%; Score 1133; DB 2; Length 231;
Best Local Similarity 94.8%; Pred. No. 6,3e-113;
Matches 219; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKDLYLYLKNSEAINSLALPPPPAVGSIAFNDQAMYEGRLLRNTER 60

```

```

Db      1 LATVATGNDTTTKPDLYLYLNKSEAINSLALPPPPAVGSIATFLNDQMYEQRLNTER 60
Oy      61 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKCHYMR 120
        |||:::|||||
Db      61 GKQAQADADLAAGVANAFAFGSPITTEKDAPALHKLNTMIEDADLATRSKCHYMR 120
Oy      121 IRPPAFYGVSTCWTTEBODKLSKNGSPSGHTSGMTATLVLAETINPORONEILKRGYEIG 180
        |||:::|||||
Db      121 IRPPAFYGVSTCWTTEBODKLSKNGSPSGHTSGMTATLVLAETINPORONEILKRGYEIG 180
        |||:::|||||
Oy      181 QSRVTCGYHWSQDVDAARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231
        |||:::|||||
Db      181 QSRVTCGYHWSQDVDAARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231
        |||:::|||||

RESULT 12
AAW71042
ID AAW71042 standard; protein; 231 AA.
AC AAW71042;
XX
XX 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
KM Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX
XX Synthetic.
XX Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65
FT Misc-difference 66 /label= A65Q
FT Misc-difference 66 /label= E66A
FT Misc-difference 69 /label= N69D
FT Misc-difference 71 /label= S71A
FT Misc-difference 72 /label= S72A
FT Misc-difference 74 /label= G74D
FT Misc-difference 92 /label= A92S
FT Misc-difference 94 /label= A94B
FT Misc-difference 116 /label= D116E
FT Misc-difference 135 /label= T135K
FT Misc-difference 136 /label= E136D
FT Misc-difference 153 /label= I153T
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y,
XX WPI; 1998-416010/36.

```

```

XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
XX provided
XX
SQ Sequence 231 AA;

```

```

Query Match 94.9%; Score 1129; DB 2; Length 231;
Best Local Similarity 94.4%; Pred. No. 1.7e-112;
Matches 218; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

```

```

Oy      1 LATVATGNDTTTKPDLYLYLNKSEAINSLALPPPPAVGSIATFLNDQMYEQRLNTER 60
        |||:::|||||
Db      1 LATVATGNDTTTKPDLYLYLNKSEAINSLALPPPPAVGSIATFLNDQMYEQRLNTER 60
        |||:::|||||
Oy      61 GKLAEDANLSSGGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKCHYMR 120
        |||:::|||||
Db      61 GKQAQADADLAAGVANAFAFGSPITTEKDAPALHKLNTMIEDAGDLATRSKCHYMR 120
        |||:::|||||
Oy      121 IRPPAFYGVSTCWTTEBODKLSKNGSPSGHTSGMTATLVLAETINPORONEILKRGYEIG 180
        |||:::|||||
Db      121 IRPPAFYGVSTCWTTEBODKLSKNGSPSGHTSGMTATLVLAETINPORONEILKRGYEIG 180
        |||:::|||||
Oy      181 QSRVTCGYHWSQDVDAARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231
        |||:::|||||
Db      181 QSRVTCGYHWSQDVDAARVVGSAVVATLTHTNPAFQOOLQAKAEFAQHOKK 231
        |||:::|||||

```

```

RESULT 13
AB061416
ID AB061416 standard; protein; 253 AA.
XX
XX AB061416;
XX
XX 29-JUL-2004 (first entry)
XX
XX Klebsiella pneumoniae polypeptide seqid 7933.
XX
XX Klebsiella pneumoniae expression vector; transcription regulatory element;
KM Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX Klebsiella pneumoniae.
XX
XX US6610836-B1.
XX
XX 26-AUG-2003.
XX
XX 27-JAN-2000; 2000US-00489039.
XX
XX 29-JAN-1999; 99US-0117747P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL, Osborne M;
XX
XX WPI; 2003-895346/82.
XX
XX N-PSDB; ACH94967.
XX

```

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.

PS Disclosure; SEQ ID NO 7933; 932pp; English.

CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention

SQ Sequence 253 AA;

Query Match 92.1%; Score 1096; DB 7; Length 253;

Best Local Similarity 92.1%; Pred. No. 6.9e-109; Mismatches 9; Indels 0; Gaps 0;

Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKRPDLYLKNSEAINSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 61

DB 25 ALVPPGNDVTTRKPDLYLKNQALDLSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 84

QY 62 KLAEDANILSSGGVANAFAFGSPITEKDAFALHKLTLNMIEDAGDLATRSADHYMRI 121

DB 85 KLAEDANILSAGVANAFSSAFSGSPITEKDAFQHLHKLTLNMIEDAGDLATRSADHYMRI 144

QY 122 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 181

DB 145 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 204

QY 182 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAFPAHOK 230

DB 205 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAFPAHOK 253

RESULT 14

AAW06458
ID AAW06458 standard; protein; 248 AA.

AC AAW06458;

DT 13-AUG-1997 (first entry)

DE Enterobacter aerogenes IFO 12010 acid phosphatase.

KW IFO 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
intermediate; pharmaceutical; intermediate.

OS Enterobacter aerogenes.

FT Key Location/Qualifiers

FT Misc-difference 92 /note="optionally replaced by another amino acid"

FT Misc-difference 171 /note="optionally replaced by another amino acid"

XX WO9637603-A1.

XX 28-NOV-1996.

XX 24-MAY-1996; 96WO-JP001402.

XX 25-MAY-1995; 95JP-00149781.

XX 26-MAR-1996; 96JP-00094680.

XX (AJIN) AJINOMOTO CO INC.

XX Minara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1997-021215/02.

XX N-PSDB; AAT45007.

PT Efficient production of nucleoside 5'-phosphate - by reaction of a
PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphate.

PS Claim 3; Page 67-68; 95pp; Japanese.

CC The present sequence is the Enterobacter aerogenes IFO 12010 acid
CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals

SQ Sequence 248 AA;

Query Match 92.0%; Score 1095; DB 2; Length 248;

Best Local Similarity 92.1%; Pred. No. 8.5e-109; Mismatches 9; Indels 0; Gaps 0;

Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKRPDLYLKNSEAINSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 61

DB 20 ALVPPGNDVTTRKPDLYLKNQALDLSLALPPPAVGSIAPLNDQAMYEQGRLLNTERG 79

QY 62 KLAEDANILSSGGVANAFAFGSPITEKDAFALHKLTLNMIEDAGDLATRSADHYMRI 121

DB 80 KLAEDANILSAGVANAFSSAFSGSPITEKDAFQHLHKLTLNMIEDAGDLATRSADHYMRI 139

QY 122 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 181

DB 140 RPPAFYGVSTCNTTTEODKLKNGSYPSGHTSIGMTALVLAELNFORONEILKRGYEIQ 199

QY 182 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAFPAHOK 230

DB 200 SRVIGCYMOSDVPDAARVGSAAVATLHTNPAFOOQLOKAKAFPAHOK 248

RESULT 15

AAW71031
ID AAW71031 standard; protein; 248 AA.

AC AAW71031;

DT 21-OCT-1998 (first entry)

DE Acid phosphatase enzyme amino acid sequence.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
intermediate.

OS Enterobacter aerogenes.

FT EP857788-A2.

PD 12-AUG-1998.

PE 20-NOV-1997; 97EP-00309365.

PR 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Minara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

XX N-PSDB; AAV43060.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.

XX Example 23; Page 44; 83pp; English.

XX The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them
 XX

SQ Sequence 248 AA;

Query Match 92.0%; Score 1095; DB 2; Length 248;
 Best Local Similarity 92.1%; Pred. No. 8.5e-109;
 Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY	2	ALVATGNDTTTTPEDLYLKNSEAINSLLALPPPPAVGSIAFLNDQAMVEQGRLLNTERG	61
DB	20	ALVPAGNDATTKPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMVEKGRLLNTERG	79
QY	62	KLAEDPANTSSGCVANAFSGAFGSPITEKDAFALHKLNTMIEDAGDLATRSKADHYMRI	121
DB	80	KLAEDPANTSSGCVANAFSGAFGSPITEKDAFALHKLNTMIEDAGDLATRSKADHYMRI	139
QY	122	RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGQ	181
DB	140	RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGQ	199
QY	182	SRVIGCYHWQSDVDARVGVSAVATLHTNPAFQOOLQKAKAEFAQHOK	230
DB	200	SRVIGCYHWQSDVDARVGVSAVATLHTNPAFQOOLQKAKAEFAQHOK	248

Search completed: March 2, 2005, 20:22:54
 Job time : 120.268 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:16:41 ; Search time 30.1961 Seconds
(without alignments)
571.065 Million cell updates/sec

Title: US-09-807-990A-124
Perfect score: 1190
Sequence: 1 LALVATGNDTTTKPDLYLK.....PAFOQOLQAKAFHQKK 231

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
 - 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1190	100.0	231	US-08-750-145A-11	Sequence 11, Appl
2	1190	100.0	231	US-08-975-698A-8	Sequence 8, Appl
3	1190	100.0	231	US-09-417-090-8	Sequence 8, Appl
4	1190	100.0	231	US-09-727-578-8	Sequence 8, Appl
5	1190	100.0	249	US-08-750-145A-10	Sequence 10, Appl
6	1190	100.0	249	US-08-975-698A-7	Sequence 7, Appl
7	1190	100.0	249	US-09-417-090-7	Sequence 7, Appl
8	1190	100.0	249	US-09-727-578-7	Sequence 7, Appl
9	1096	92.1	253	US-09-489-039A-7933	Sequence 7933, Ap
10	1096	92.0	248	US-08-750-145A-20	Sequence 20, Appl
11	1095	92.0	248	US-08-975-698A-24	Sequence 24, Appl
12	1095	92.0	248	US-09-417-090-24	Sequence 24, Appl
13	1095	92.0	248	US-09-727-578-24	Sequence 24, Appl
14	1080	90.8	248	US-08-750-145A-22	Sequence 22, Appl
15	1080	90.8	248	US-08-975-698A-26	Sequence 26, Appl
16	1080	90.8	248	US-09-417-090-26	Sequence 26, Appl
17	1080	90.8	248	US-09-727-578-26	Sequence 26, Appl
18	986	82.9	248	US-08-750-145A-18	Sequence 18, Appl
19	986	82.9	248	US-08-975-698A-22	Sequence 22, Appl
20	986	82.9	248	US-09-417-090-22	Sequence 22, Appl
21	986	82.9	248	US-09-727-578-22	Sequence 22, Appl
22	969	81.4	249	US-08-750-145A-3	Sequence 3, Appl
23	969	81.4	249	US-08-975-698A-3	Sequence 3, Appl
24	969	81.4	249	US-09-417-090-3	Sequence 3, Appl
25	969	81.4	249	US-09-727-578-3	Sequence 3, Appl
26	962	80.8	229	US-08-750-145A-4	Sequence 4, Appl
27	962	80.8	229	US-08-975-698A-4	Sequence 4, Appl

28	962	80.8	229	US-09-417-090-4	Sequence 4, Appl
29	962	80.8	229	US-09-727-578-4	Sequence 4, Appl
30	768	64.5	244	US-08-750-145A-24	Sequence 24, Appl
31	768	64.5	244	US-08-975-698A-28	Sequence 28, Appl
32	768	64.5	244	US-09-417-090-28	Sequence 28, Appl
33	768	64.5	244	US-09-727-578-28	Sequence 28, Appl
34	312	26.2	252	US-07-717-332D-2	Sequence 2, Appl
35	191	16.1	428	US-09-489-039A-10941	Sequence 10941, A
36	181	15.2	943	US-09-540-236-3458	Sequence 3458, Ap
37	173.5	14.6	253	US-09-252-991A-28557	Sequence 28557, A
38	147	12.4	987	US-09-543-681A-7785	Sequence 7785, Ap
39	92.5	7.8	159	US-09-602-787A-102	Sequence 102, App
40	90.5	7.6	244	US-09-252-991A-21937	Sequence 21937, A
41	89.5	7.5	244	US-09-543-681A-4595	Sequence 4595, Ap
42	88.5	7.4	824	US-09-711-164-377	Sequence 377, App
43	88.5	7.4	1627	US-09-902-540-11280	Sequence 11280, A
44	85.5	7.2	187	US-09-328-352-7918	Sequence 7918, Ap
45	85.5	7.2	816	US-09-540-236-3443	Sequence 3443, Ap

ALIGNMENTS

RESULT 1
US-08-750-145A-11
Sequence 11, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blactae
STRAIN: JCM 1650

US-08-750-145A-11

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTTPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTER 60
DB 1 LALVATGNDTTTTPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTER 60
QY 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSADHYMR 120
DB 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSADHYMR 120
QY 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELG 180
DB 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELG 180
QY 181 OSRVICGYHOSDVDAARVGSAAVATLTNPAPFOOLQAKAEFAQHOKK 231
DB 181 OSRVICGYHOSDVDAARVGSAAVATLTNPAPFOOLQAKAEFAQHOKK 231

RESULT 2

US-08-975-698A-8
Sequence 8, Application US/08975698A
Patent No. 6015697

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid

MOLECULE TYPE: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650

US-08-975-698A-8

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTTPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTER 60
DB 1 LALVATGNDTTTTPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTER 60
QY 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSADHYMR 120
DB 61 GKLAADANLSSGGVANAFAFGSPITEKAPALHKLITNMIEDAGDLATRSADHYMR 120
QY 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELG 180
DB 121 IRPFAVGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELG 180
QY 181 OSRVICGYHOSDVDAARVGSAAVATLTNPAPFOOLQAKAEFAQHOKK 231
DB 181 OSRVICGYHOSDVDAARVGSAAVATLTNPAPFOOLQAKAEFAQHOKK 231

RESULT 3

US-09-417-090-8
Sequence 8, Application US/09417090
Patent No. 6207435

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid

MOLECULE TYPE: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650

US-09-417-090-8

Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTTPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTER 60
DB 1 LALVATGNDTTTTPDLYLKNSEAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTER 60

Db 1 LALVATGNDTTTCKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Qy 61 GKLAEDANLSSGGVANA FSGAFGSPITEKDA PALHKLTTNMIEDAGDLATRS AKDHYMR 120
Db 61 GKLAEDANLSSGGVANA FSGAFGSPITEKDA PALHKLTTNMIEDAGDLATRS AKDHYMR 120
Qy 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Db 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Qy 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFOOQLOKAKAEFAQHOKK 231
Db 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFOOQLOKAKAEFAQHOKK 231

RESULT 4
US-09-727-578-8
Sequence 8, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-8
Query Match 100.0%; Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.9e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LALVATGNDTTTCKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Db 1 LALVATGNDTTTCKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Qy 61 GKLAEDANLSSGGVANA FSGAFGSPITEKDA PALHKLTTNMIEDAGDLATRS AKDHYMR 120

Db 61 GKLAEDANLSSGGVANA FSGAFGSPITEKDA PALHKLTTNMIEDAGDLATRS AKDHYMR 120
Qy 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Db 121 IRPPAFYGVSTCNTTEODKLSKNSGSPSGHTSIGMATAVLAEINPQRONEILRGVELG 180
Qy 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFOOQLOKAKAEFAQHOKK 231
Db 181 OSRVICGYHMOSDVDAARVGSAAVATLHTNPAFOOQLOKAKAEFAQHOKK 231

RESULT 5
US-08-750-145A-10
Sequence 10, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-750-145A-10
Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LALVATGNDTTTCKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 60
Db 19 LALVATGNDTTTCKDLYYLKNSSEAINSLALLPPPAVGSIAFLNDQAMYEGRLLRNTER 78
Qy 61 GKLAEDANLSSGGVANA FSGAFGSPITEKDA PALHKLTTNMIEDAGDLATRS AKDHYMR 120

Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGDLATRSKDHMR 138
QY 121 IRPFAFYGVSTCNTTEBDKLSKNGSYSGHTSIGMATALVLAETINPORONEILKRGYELG 180
Db 139 IRPFAFYGVSTCNTTEBDKLSKNGSYSGHTSIGMATALVLAETINPORONEILKRGYELG 198
QY 181 QSRVTCGYHMQSDVDARVGSAAVATLHTNPAFQOOLQAKAEFAHQK 231
Db 199 QSRVTCGYHMQSDVDARVGSAAVATLHTNPAFQOOLQAKAEFAHQK 249

RESULT 6

US-08-975-698A-7
Sequence 7, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-975-698A-7

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTDPDLYLKNSEALNSIALLPPEPAVGSIAFLNDQAMYEQGRLLRNTER 60
Db 19 LALVATGNDTTTDPDLYLKNSEALNSIALLPPEPAVGSIAFLNDQAMYEQGRLLRNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGDLATRSKDHMR 120
Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGDLATRSKDHMR 138
QY 121 IRPFAFYGVSTCNTTEBDKLSKNGSYSGHTSIGMATALVLAETINPORONEILKRGYELG 180
Db 139 IRPFAFYGVSTCNTTEBDKLSKNGSYSGHTSIGMATALVLAETINPORONEILKRGYELG 198

QY 181 QSRVTCGYHMQSDVDARVGSAAVATLHTNPAFQOOLQAKAEFAHQK 231
Db 199 QSRVTCGYHMQSDVDARVGSAAVATLHTNPAFQOOLQAKAEFAHQK 249

RESULT 7

US-09-417-090-7
Sequence 7, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-417-090-7

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTDPDLYLKNSEALNSIALLPPEPAVGSIAFLNDQAMYEQGRLLRNTER 60
Db 19 LALVATGNDTTTDPDLYLKNSEALNSIALLPPEPAVGSIAFLNDQAMYEQGRLLRNTER 78
QY 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGDLATRSKDHMR 120
Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLITNMIEDAGDLATRSKDHMR 138
QY 121 IRPFAFYGVSTCNTTEBDKLSKNGSYSGHTSIGMATALVLAETINPORONEILKRGYELG 180
Db 139 IRPFAFYGVSTCNTTEBDKLSKNGSYSGHTSIGMATALVLAETINPORONEILKRGYELG 198
QY 181 QSRVTCGYHMQSDVDARVGSAAVATLHTNPAFQOOLQAKAEFAHQK 231

Db 199 OSRVICGYHMOQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAEPAHQOKK 249

RESULT 8
US-09-727-578-7

; Sequence 7, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia biattaee
; STRAIN: JCM 1650
; US-09-727-578-7

Query Match 100.0%; Score 1190; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 3,3e-130;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LALVATGNDTTTKPDLVYLKNSAENSLALLPPPPAVGSIAFLNDQAYEGRLRNTER 60
|||
Db 19 LALVATGNDTTTKPDLVYLKNSAENSLALLPPPPAVGSIAFLNDQAYEGRLRNTER 78
|||
Qy 61 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 120
|||
Db 79 GKLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 138
|||
Qy 121 IRPFAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPPQRNEILKRGYELG 180
|||
Db 139 IRPFAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPPQRNEILKRGYELG 198
|||
Qy 181 OSRVICGYHMOQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAEPAHQOKK 231
|||
Db 199 OSRVICGYHMOQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAEPAHQOKK 249
|||

RESULT 9
US-09-489-039A-7933

; Sequence 7933, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7933
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-7933

Query Match 92.1%; Score 1096; DB 4; Length 253;
Best Local Similarity 92.1%; Pred. No. 3.1e-119;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 2 ALVATGNDTTTKPDLVYLKNSAENSLALLPPPPAVGSIAFLNDQAYEGRLRNTER 61
|||
Db 25 ALVPPGNDVTTKPDLYLTNQAIDSLALLPPPPAVGSIAFLNDQAYEGRLRNTER 84
|||
Qy 62 KLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 121
|||
Db 85 KLAEDANLSSGGVANAFAFGSPITEKDA PALHKLTTNMIEDAGDLATRSADHYMR 144
|||
Qy 122 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPPQRNEILKRGYELG 181
|||
Db 145 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGWATLVLAELNPPQRNEILKRGYELG 204
|||
Qy 182 SRVICGYHMOQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAEPAHQOKK 230
|||
Db 205 SRVICGYHMOQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAEPAHQOKK 253
|||

RESULT 10
US-08-750-145A-20

; Sequence 20, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: UTAGAWA, Takashi
; APPLICANT: YAMADA, Hideaki
; APPLICANT: ASANO, Yasuhisa
; TITLE OF INVENTION: Method for Producing Nucleoside-5'-
; TITLE OF INVENTION: Phosphate Ester
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,145A
; FILING DATE: 01-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-149781
; FILING DATE: 05-May-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8-094680
 FILING DATE: 26-Mar-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: NORMAN F. OBLON
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Enterobacter aerogenes
 STRAIN: IFO 12010
 US-08-750-145A-20

Query Match 92.0%; Score 1095; DB 3; Length 248;
 Best Local Similarity 92.1%; Pred. No. 3.9e-119;
 Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYYKNSAINSIALPPPPAVGSIAFLNDQAMYEQRLNTERG 61
 DB 20 ALVPAGNDATTKPDLYYKNAQAIIDSLALPPPEVGSIAFLNDQAMYEQRLNTERG 79
 QY 62 KLAEDANLSSGVANAFSGAFSGSPITEKDAPOHLKLTNMIEDGDLATRSADHYMRI 121
 DB 80 KLAEDANLSSGVANAFSGAFSGSPITEKDAPOHLKLTNMIEDGDLATRSADHYMRI 139
 QY 122 RPPAFYGVSTCNTTEQDKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
 DB 140 RPPAFYGVSTCNTTEQDKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 199
 QY 182 SRVIGYHMQSDVDAAVGSAYVATHTNPAPFOOLQKAKDEFKQK 230
 DB 200 SRVIGYHMQSDVDAAVGSAYVATHTNPAPFOOLQKAKDEFKQK 248

RESULT 11
 US-08-975-698A-24
 Sequence 24, Application US/08975698A
 Patent No. 6015697
 GENERAL INFORMATION:
 APPLICANT: MIHARA, YASUHIRO
 APPLICANT: UTAGAWA, TAKASHI
 APPLICANT: YAMADA, HIDEAKI
 APPLICANT: ASANO, YASUHIISA
 TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,698A
 FILING DATE: 21-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Enterobacter aerogenes
 STRAIN: IFO 12010
 US-08-975-698A-24

Query Match 92.0%; Score 1095; DB 3; Length 248;
 Best Local Similarity 92.1%; Pred. No. 3.9e-119;
 Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYYKNSAINSIALPPPPAVGSIAFLNDQAMYEQRLNTERG 61
 DB 20 ALVPAGNDATTKPDLYYKNAQAIIDSLALPPPEVGSIAFLNDQAMYEQRLNTERG 79
 QY 62 KLAEDANLSSGVANAFSGAFSGSPITEKDAPOHLKLTNMIEDGDLATRSADHYMRI 121
 DB 80 KLAEDANLSSGVANAFSGAFSGSPITEKDAPOHLKLTNMIEDGDLATRSADHYMRI 139
 QY 122 RPPAFYGVSTCNTTEQDKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
 DB 140 RPPAFYGVSTCNTTEQDKLSKNGSPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 199
 QY 182 SRVIGYHMQSDVDAAVGSAYVATHTNPAPFOOLQKAKDEFKQK 230
 DB 200 SRVIGYHMQSDVDAAVGSAYVATHTNPAPFOOLQKAKDEFKQK 248

RESULT 12
 US-09-417-090-24
 Sequence 24, Application US/09417090
 Patent No. 6207435
 GENERAL INFORMATION:
 APPLICANT: MIHARA, YASUHIRO
 APPLICANT: UTAGAWA, TAKASHI
 APPLICANT: YAMADA, HIDEAKI
 APPLICANT: ASANO, YASUHIISA
 TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/417,090
 FILING DATE: 13-OCT-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975,698
 FILING DATE: 21-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-417-090-24

Query Match 92.0%; Score 1095; DB 3; Length 248;
Best Local Similarity 92.1%; Pred. No. 3.9e-119;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSAINSIALPPPPAVGSIAFLNDQAMTEQGLLNTERG 61
DB 20 ALVAGNDATTKPDLYLKNAQAIIDSLALPPPEVGSIAPLNDQAMEKGRLLNTERG 79
QY 62 KLAADANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 121
DB 80 KLAADANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIQ 181
DB 140 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIQ 199
QY 182 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAFPAKHOK 230
DB 200 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAFPAKHOK 248

RESULT 13
US-09-727-578-24
Sequence 24, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 92.0%; Score 1095; DB 3; Length 248;
Best Local Similarity 92.1%; Pred. No. 3.9e-119;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSAINSIALPPPPAVGSIAFLNDQAMTEQGLLNTERG 61
DB 20 ALVAGNDATTKPDLYLKNAQAIIDSLALPPPEVGSIAPLNDQAMEKGRLLNTERG 79
QY 62 KLAADANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 121
DB 80 KLAADANLSSGVANAFSSAFSGSPITEKDAPOHLKLLTNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIQ 181
DB 140 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIQ 199
QY 182 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAFPAKHOK 230
DB 200 SRVIGYHWSQDVDAARVGSAAVATLHTNPAFOOOLOKAKAFPAKHOK 248

RESULT 14
US-08-750-145A-22
Sequence 22, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-750-145A-22

Query Match 90.8%; Score 1080; DB 3; Length 248;
Best Local Similarity 90.8%; Pred. No. 2.2e-117;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAMVEQRLRLRTERG 61
DB 20 ALVPAGNDATTKRDLYLKNAQALDSIALLPPEVSGIAFLNDQAMVEQRLRLRTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSAGGVANAFSAFGSPISEKDPALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
DB 140 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELG 199
QY 182 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKDEPAKQK 230
DB 200 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKDEPAKQK 248

RESULT 15
US-08-975-698A-26
Sequence 26, Application US/08975698A

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-975-698A-26

Query Match 90.8%; Score 1080; DB 3; Length 248;
Best Local Similarity 90.8%; Pred. No. 2.2e-117;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTTKPDLYLKNSSEAINSLALPPPPAVGSIAPLNDQAMVEQRLRLRTERG 61
DB 20 ALVPAGNDATTKRDLYLKNAQALDSIALLPPEVSGIAFLNDQAMVEQRLRLRTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSAGGVANAFSAFGSPISEKDPALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELGQ 181
DB 140 RPPAFYGVSTCNTTEODKLSNGSYPSGHTSIGMATLVLAETNPORONEILKRGYELG 199
QY 182 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKDEPAKQK 230
DB 200 SRVTCGYHMOQSDVDAAVVGSAVVATLHTNPAFQOOLQKAKDEPAKQK 248

Search completed: March 2, 2005, 20:28:50
Job time : 31.1961 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:26:57 ; Search time 87.5686 Seconds

(without alignments)
865.359 Million cell updates/sec

Title: US-09-807-990A-124

Perfect score: 1190

Sequence: 1 LALVATGNDTFTTKPDLYLK.....PAFQOOLQKAKAFHQHKK 231

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

```
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1190	100.0	231	9	US-09-727-578-8
2	1190	100.0	249	9	US-09-727-578-7
3	1095	97.0	248	9	US-09-727-578-24
4	1080	90.8	248	9	US-09-727-578-26
5	986	82.9	248	9	US-09-727-578-22
6	969	81.4	249	9	US-09-727-578-3
7	965	81.1	229	16	US-10-220-481-116
8	962	80.8	229	9	US-09-727-578-4
9	768	64.5	244	9	US-09-738-626-4817
10	143	12.0	622	9	US-09-738-626-4817
11	109	9.2	414	16	US-10-437-963-165801
12	99.5	8.4	353	15	US-10-374-780A-1704
13	99.5	8.4	353	16	US-10-437-963-194124

14	96	8.1	178	15	US-10-282-122A-77490	Sequence 77490, A
15	95.5	8.0	2135	16	US-10-437-963-122794	Sequence 122794, A
16	93.5	7.9	704	14	US-10-213-990-21	Sequence 21, Appl
17	93.5	7.9	1610	15	US-10-369-493-3448	Sequence 3448, Ap
18	93	7.8	608	15	US-10-369-493-5228	Sequence 5228, Ap
19	92.5	7.8	159	9	US-09-738-626-6679	Sequence 6679, Ap
20	92.5	7.8	159	15	US-10-627-476-102	Sequence 102, App
21	91	7.6	201	14	US-10-156-761-7677	Sequence 7677, App
22	90.5	7.6	437	15	US-10-282-122A-66585	Sequence 66585, A
23	90	7.6	305	15	US-10-369-493-3179	Sequence 3179, Ap
24	88.5	7.4	168	9	US-09-738-626-6676	Sequence 6676, Ap
25	88.5	7.4	824	14	US-10-287-274-377	Sequence 377, App
26	88.5	7.4	824	15	US-10-282-122A-42600	Sequence 42600, A
27	88	7.4	921	14	US-10-281-866-2	Sequence 2, Appl1
28	87	7.3	408	15	US-10-369-493-9754	Sequence 9754, Ap
29	85.5	7.2	221	15	US-10-282-122A-69103	Sequence 69103, A
30	85.5	7.2	774	15	US-10-282-122A-63166	Sequence 63166, A
31	85	7.1	766	14	US-10-317-832-120	Sequence 120, App
32	84.5	7.1	4317	15	US-10-282-122A-67862	Sequence 67862, A
33	84	7.1	278	9	US-09-765-272-94	Sequence 94, Appl1
34	84	7.1	571	9	US-09-765-272-4	Sequence 4, Appl1
35	84	7.1	2004	17	US-10-472-928-2306	Sequence 2306, Ap
36	83.5	7.0	260	16	US-10-408-765A-1756	Sequence 1756, Ap
37	83.5	7.0	515	15	US-10-389-566-351	Sequence 351, App
38	83	7.0	268	15	US-10-282-122A-63138	Sequence 63138, A
39	82.5	6.9	402	14	US-10-081-051-16	Sequence 16, Appl1
40	82	6.9	410	15	US-10-282-122A-45687	Sequence 45687, A
41	81.5	6.8	198	15	US-10-282-122A-50258	Sequence 50258, A
42	81.5	6.8	265	15	US-10-424-599-243256	Sequence 243256, A
43	81.5	6.8	349	15	US-10-150-048-4	Sequence 4, Appl1
44	81.5	6.8	518	9	US-09-738-626-4323	Sequence 4323, Ap
45	81	6.8	20	9	US-09-727-578-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-727-578-8
Sequence 8, Application US/09727578
; Publication No. US2002004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAHAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ORION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727, 578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975, 698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ORION, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-6

Query Match 100.0%; Score 1190; DB 9; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.5e-117;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLVYLKNSSEAINSLALLPPPPAVGSIATFNDQMYEQGRLNTER 60
DB 1 LALVATGNDTTTKPDLVYLKNSSEAINSLALLPPPPAVGSIATFNDQMYEQGRLNTER 60
QY 61 GKLAEDANLSSGGVNAFSGAFSGPITEKQAPALHKLITNMTEDAGDLATRSKDHMYR 120
DB 61 GKLAEDANLSSGGVNAFSGAFSGPITEKQAPALHKLITNMTEDAGDLATRSKDHMYR 120
QY 121 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
DB 121 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
QY 181 QSRVTCGYHWSQVDVDAARVGSAAVATLHTNPAFOQLQKAKAFQHQK 231
DB 181 QSRVTCGYHWSQVDVDAARVGSAAVATLHTNPAFOQLQKAKAFQHQK 231

RESULT 2
US-09-727-578-7
Sequence 7, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-7

Query Match 100.0%; Score 1190; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LALVATGNDTTTKPDLVYLKNSSEAINSLALLPPPPAVGSIATFNDQMYEQGRLNTER 60
DB 19 LALVATGNDTTTKPDLVYLKNSSEAINSLALLPPPPAVGSIATFNDQMYEQGRLNTER 78
QY 61 GKLAEDANLSSGGVNAFSGAFSGPITEKQAPALHKLITNMTEDAGDLATRSKDHMYR 120
DB 79 GKLAEDANLSSGGVNAFSGAFSGPITEKQAPALHKLITNMTEDAGDLATRSKDHMYR 138
QY 121 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYEIG 180
DB 139 IRPFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYEIG 198
QY 181 QSRVTCGYHWSQVDVDAARVGSAAVATLHTNPAFOQLQKAKAFQHQK 231
DB 199 QSRVTCGYHWSQVDVDAARVGSAAVATLHTNPAFOQLQKAKAFQHQK 249

RESULT 3
US-09-727-578-24
Sequence 24, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 92.0%; Score 1095; DB 9; Length 248;
Best Local Similarity 92.1%; Pred. No. 26-107;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTERG 61
DB 20 ALVPAQNDATTKPDLYLKNAQIDSLALPPPEVGSIAFLNDQAMTEKGRLLNTERG 79
QY 62 KLAADANLSSGVANAFSAGFSPITEKDA PALHKLNTMI EDAGDLATRS AKDHVRI 121
DB 80 KLAADANLSSGVANAFSAGFSPITEKDA PALHKLNTMI EDAGDLATRS AKDHVRI 139
QY 122 RPFAYGVSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELG 181
DB 140 RPFAYGVSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELG 199
QY 182 SRVIGYHMQSDVDARVGSAAVATLTHTNPAFOQOLQKAKAEPAQHOK 230
DB 200 SRVIGYHMQSDVDARVGSAAVATLTHTNPAFOQOLQKAKAEPAKHOK 248

RESULT 4

US-09-727-578-26
Sequence 26, Application US/09727578
Publication No. US20020004590A1

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-09-727-578-26

Query Match 90.8%; Score 1080; DB 9; Length 248;
Best Local Similarity 90.8%; Pred. No. 7,7e-106;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMTEQGRLLNTERG 61
DB 20 ALVPAQNDATTKPDLYLKNAQIDSLALPPPEVGSIAFLNDQAMTEKGRLLNTERG 79
QY 62 KLAADANLSSGVANAFSAGFSPITEKDA PALHKLNTMI EDAGDLATRS AKDHVRI 121
DB 80 KLAADANLSSGVANAFSAGFSPITEKDA PALHKLNTMI EDAGDLATRS AKDHVRI 139
QY 122 RPFAYGVSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELG 181
DB 140 RPFAYGVSTCNTTEBODKLSKNGSPSGHTSIGMATLVLAELNFORONEILKRGYELG 199
QY 182 SRVIGYHMQSDVDARVGSAAVATLTHTNPAFOQOLQKAKAEPAQHOK 230
DB 200 SRVIGYHMQSDVDARVGSAAVATLTHTNPAFOQOLQKAKAEPAKHOK 248

RESULT 5

US-09-727-578-22
Sequence 22, Application US/09727578
Publication No. US20020004590A1

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Providencia stuartii
STRAIN: ATCC 29851
US-09-727-578-22

Query Match 82.9%; Score 986; DB 9; Length 248;
Best Local Similarity 81.2%; Pred. No. 7.2e-96;
Matches 186; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSKSEAINSLALLPPPPAVGSIAPLNDQAMYEQGLRNTERG 61
DB 20 AAIPEGNDATTKPDLYLKNSQALDSLALPPPEVGSILFLNDQAMYEKGRLRNTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 121
DB 80 EQAKADADLAAGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 139
QY 122 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLAELNPNORNEILKRGYELG 181
DB 140 RPPAFYGVATCNTDQDKLSKNGSYPSGHTSIGWATLVLAELNPNQDALILRGYELG 199
QY 182 SRVTCGYHMOSDVAARIVGSAVAATLHTNPAFOOQLAKAKAEPAQHSQK 230
DB 200 SRVTCGYHMOSDVAARIVGSAVAATLHTNPAFOOQLAKAKAEPAQHSQK 248

RESULT 6
US-09-727-578-3
; Sequence 3, Application US/09727578
; Publication No. US2002004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: *Morganella morganii*
; STRAIN: NCIMB 10466
US-09-727-578-3

Query Match 81.4%; Score 969; DB 9; Length 249;
Best Local Similarity 79.2%; Pred. No. 4.6e-94;

Matches 183; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 LALVATGNDTTKPDLYLKNSKSEAINSLALLPPPPAVGSIAPLNDQAMYEQGLRNTERG 60
DB 19 LAAIPEGNDATTKPDLYLKNSQALDSLALPPPEVGSILFLNDQAMYEKGRLRNTERG 78
QY 61 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 120
DB 79 GKQADADLAAGVATAFSGAFGYITEKDSPELYKLTNMIEDAGDLATRSAXDHYMR 138
QY 121 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLAELNPNORNEILKRGYELG 180
DB 139 RPPAFYGVETCNTDQDKLSKNGSYPSGHTSIGWATLVLAELNPNQDALILRGYELG 198
QY 181 SRVTCGYHMOSDVAARIVGSAVAATLHTNPAFOOQLAKAKAEPAQHSQK 231
DB 199 SRVTCGYHMOSDVAARIVGSAVAATLHTNPAFOOQLAKAKAEPAQHSQK 249

RESULT 7
US-10-220-481-116
; Sequence 116, Application US/10220481
; Publication No. US20040110670A1
; GENERAL INFORMATION:
; APPLICANT: ARICO, Maria B., et al.
; TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
; FILE REFERENCE: CHIR-15883/01US
; CURRENT APPLICATION NUMBER: US/10/220,481
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/IB01/00452
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 633
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 116
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel protein
US-10-220-481-116

Query Match 81.1%; Score 965; DB 16; Length 249;
Best Local Similarity 79.1%; Pred. No. 1.2e-93;
Matches 182; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSKSEAINSLALLPPPPAVGSIAPLNDQAMYEQGLRNTERG 61
DB 20 AAIPEGNDATTKPDLYLKNSQALDSLALPPPEVGSILFLNDQAMYEKGRLRNTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITEKDPALHKLITNMIEDAGDLATRSAXDHYMR 121
DB 80 KQADADADLAAGVATAFSGAFGYITEKDSPELYKLTNMIEDAGDLATRSAXDHYMR 139
QY 122 RPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGWATLVLAELNPNORNEILKRGYELG 181
DB 140 RPPAFYGVETCNTDQDKLSKNGSYPSGHTSIGWATLVLAELNPNQDALILRGYELG 199
QY 182 SRVTCGYHMOSDVAARIVGSAVAATLHTNPAFOOQLAKAKAEPAQHSQK 231
DB 200 SRVTCGYHMOSDVAARIVGSAVAATLHTNPAFOOQLAKAKAEPAQHSQK 249

RESULT 8
US-09-727-578-4
; Sequence 4, Application US/09727578
; Publication No. US2002004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER

```

;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT, P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Morganella morganii
; STRAIN: NCIMB 10466
; US-09-727-578-4
;
; Query Match 80.8%; Score 962; DB 9; Length 229;
; Best Local Similarity 79.4%; Pred. No. 2.3e-93;
; Matches 181; Conservative 20; Mismatches 27; Indels 0; Gaps 0;
;
Qy 4 VATGDDTTKPDLYYLNKSEAINSLALLPPPPVAGSIAPLNDQAMYEQRLNTERGKL 63
Db 2 IPAGDATTKPDLYYLNKQEAIDSLKLPPEVGSIOFLNDQAMTEKRLNTERGKQ 61
Qy 64 AADANLSSGGVANA FSGAFSGPITEKDA PALHKLITNMIEDAGDLATRSADHYMRIRP 123
Db 62 AOADADLAAGVATAFSGAFGYPITEKDSPELYKLTNMIEDAGDLATRSADHYMRIRP 121
Qy 124 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPPORONELIKRGYELGQSR 183
Db 122 FAFYGTETCNTDQDKLSTNGSYPSGHTSIGWATLVLAELVNPADQDLIERGYOLGQSR 181
Qy 184 VICGYHWSQDVDAARVGSAAVATLTNPAFOOQLKAKAEPAHQK 231
Db 182 VICGYHWSQDVDAARIVGSAVAATLHSDPAFOQLAKAQEPKQSK 229
;
; RESULT 9
; US-09-727-578-28
; Sequence 28, Application US/09727578
; Publication No. US2002004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT, P. C.

```

```

;
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Serratia ficaria
; STRAIN: IAM 13540
; US-09-727-578-28
;
; Query Match 64.5%; Score 768; DB 9; Length 244;
; Best Local Similarity 66.8%; Pred. No. 9.4e-73;
; Matches 145; Conservative 29; Mismatches 43; Indels 0; Gaps 0;
;
Qy 9 DTTTKPDLYYLNKSEAINSLALLPPPPVAGSIAPLNDQAMYEQRLNTERGKLAADA 68
Db 23 DVTTHPEVYFLQESQSIDSLALLPPPPMDSIDFLNDQAYDAGKIVNTFRGKQAYDDA 82
Qy 69 NLSSGGVANA FSGAFSGPITEKDA PALHKLITNMIEDAGDLATRSADHYMRIRPFAFY 128
Db 83 HVAAGGVAAAFSNFAGIEAQRKPELFKLWKREKEDAGDLATRSADHYMRIRPFAFY 142
Qy 129 VSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPPORONELIKRGYELGQSRVIGY 188
Db 143 EATCRPDESESTLSKNGSYPSGHTTIGWATLVLAELNPPARQGEILRGYDMGQSRVIGY 202
Qy 189 HWQSDVDAAARVGSAAVATLTNPAFOOQLKAKAEF 225
Db 203 HWQSDVTAARMAASAMVRLHAEPFAAQLOKADDEF 239
;
; RESULT 10
; US-09-738-626-4817
; Sequence 4817, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125

```

[illegible]

Db 131 CNDQATPSNPPTTTRAR---YGGGVRYLPAVSPSPCAQRRRASSKNGGGGSSSA 186
 Oy 154 G-WATLALAEINPQROHEILKRGVLEGSRYICGYHMSDVARVGSANVALTLHNP 212
 Db 187 APYAEHIIAE--RRRREKINQRIEL--STVIFGL---KKMDKATITLSDAV----- 231
 Oy 213 AFOOOLQAKAEFAOHQ 229
 Db 232 RYVKEMQKLSLEOHQ 248

RESULT 13

US-10-437-963-194124
 ; Sequence 194124, Application US/10437963
 ; Publication No. US2004023343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 194124
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_90197C.1.pep
 ; US-10-437-963-194124

Query Match 8.4%; Score 99.5; DB 16; Length 353;
 Best Local Similarity 24.5%; Pred. No. 0.13;
 Matches 63; Conservative 31; Mismatches 92; Indels 71; Gaps 13;
 Oy 23 EAINSLALP--PPAVGSIAFLNDQAWYEGRLRN---TERGLAED-----AN 69
 Db 13 ETLQHLPLPATPPAGGYA--GNATPPLQALRESSVSONGMAPEPTAHGHRASN 70
 Oy 70 LSSGCVANAFSGAFSPITEKDA-----PALHKLITNMTD 105
 Db 71 SMSGSDTDSVSGGGGAVMEHDMSTSPNSVRCACAGGGGGGGLWTFVSNMFSAMTOP 130
 Oy 106 AGDLATRSKADHYMRIRPPAYG-----VSTCNTTEDKLSK--NGSYPSGHTSI 153
 Db 131 CNDQATPSNPPTTTRAR---YGGGVRYLPAVSPSPCAQRRRASSKNGGGGSSSA 186
 Oy 154 G-WATLALAEINPQROHEILKRGVLEGSRYICGYHMSDVARVGSANVALTLHNP 212
 Db 187 APYAEHIIAE--RRRREKINQRIEL--STVIFGL---KKMDKATITLSDAV----- 231
 Oy 213 AFOOOLQAKAEFAOHQ 229
 Db 232 RYVKEMQKLSLEOHQ 248

RESULT 14
 US-10-282-122A-77490
 ; Sequence 77490, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Hasebeck, Robert

APPLICANT: Ohlsen, Kari
 APPLICANT: Zykand, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: EUTRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 77490
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: Vibrio cholerae
 ; US-10-282-122A-77490

Query Match 8.1%; Score 96; DB 15; Length 178;
 Best Local Similarity 31.0%; Pred. No. 0.11;
 Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;
 Oy 115 KDHYMRIRPPAYGVSTCNTTEDKLSKNGSYPSGHTSIGWATLALAEINPQROHEILK 174
 Db 81 KNSFORRRPCELSALVTAIYTPSDRY---SLPSGHTAAAFVWATLIGYIPHWYAVALC 136
 Oy 175 RGYELGOSRYICGYHMSDVARVGS 201
 Db 137 WAGLIGLARVILGVHPLSDVIAALIG 163

RESULT 15
 US-10-437-963-122794
 ; Sequence 122794, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:51 ; Search time 25.6667 Seconds
(without alignments)
865.951 Million cell updates/sec

Title: US-09-807-990A-124
Perfect score: 1190
Sequence: 1 LAIVATGNDTTKPDLYLK.....PAFQQQLQKAAEPAQHOKK 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	82.9	248	1	PROFCS
2	969	81.4	249	1	acid phosphatase (
3	485	40.8	250	1	acid phosphatase (
4	477	40.1	250	1	acid phosphatase (
5	329	27.6	264	1	acid phosphatase (
6	274.5	23.1	258	2	acid phosphatase (
7	189.5	15.9	2314	2	hypothetical prote
8	172.5	14.5	241	2	probable acid phos
9	157	13.2	591	2	uncharacterized pr
10	141	11.8	660	2	serine proteinase
11	141	11.8	660	2	vanadium chlorop
12	105	8.8	145	2	conserved hypothet
13	99.5	8.4	259	2	conserved hypothet
14	96	8.1	178	2	protein B0205.3 (1
15	93	7.8	608	2	hypothetical prote
16	91	7.6	217	2	conserved hypothet
17	91	7.6	242	2	hypothetical prote
18	90.5	7.6	437	2	hypothetical prote
19	89.5	7.5	1157	2	PAS1 protein - yea
20	88.5	7.4	824	2	ATP-dependent heli
21	88	7.4	589	2	hypothetical prote
22	87.5	7.4	320	2	hypothetical prote
23	86.5	7.3	368	2	probable porin Vc1
24	86.5	7.3	824	2	helicase, ATP-depe
25	86.5	7.3	824	2	ATP-dependent heli
26	86	7.2	292	2	phosphatidylylase
27	85.5	7.2	390	2	2-C-methyl-D-eryth
28	85	7.1	725	2	vach-like (shigel
29	85	7.1	766	2	P element transpos

30	84	7.1	474	2	AE3426	mannose-1-phosphat
31	84	7.1	2004	2	P95133	immunoglobulin A1
32	83	7.0	548	2	AC0871	probable integrase
33	83	7.0	753	2	S22802	transposase (clone
34	83	7.0	1588	2	A86036	probable adhesin Z
35	83	7.0	1588	2	H91188	probable adhesin E
36	82.5	6.9	525	2	C82914	conserved hypothet
37	82.5	6.9	561	1	VCN241	cell fusion glycop
38	82.5	6.9	921	2	A54139	Na+/Ca2+-exchangin
39	82	6.9	562	2	S46281	P element - fruit
40	81	6.8	247	2	T35796	probable integral
41	81	6.8	490	2	S75539	hypothetical prote
42	81	6.8	726	2	D97012	probable processiv
43	80.5	6.8	218	2	E97497	22k outer membrane
44	80.5	6.8	218	2	AB2716	outer membrane pro
45	80.5	6.8	272	1	G82076	3',5'-cyclic-nucle

ALIGNMENTS

RESULT 1
acid phosphatase (EC 3.1.3.2) - Providencia stuartii
C:Species: Providencia stuartii
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: S19888
R:Riccio, M.L.; Lombardi, G.; Chiesurin, A.; Satta, G.
A:Reference number: S19888
A:Accession: S19888
A:Molecule type: DNA
A:Residues: 1-248 <RIC>
A:Cross-references: UNIPROT: P26975; EMBL: X64820; NID: g45861; PID: g45862
C:Genetics:
A:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoster hydrolase
F:103-222/Domain: glucose-6-phosphatase catalytic domain homology <GRH>

Query Match 82.9%; Score 986; DB 1; Length 248;
Best Local Similarity 81.2%; Pred. No. 4.5e-80;
Matches 186; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY	2	LAIVATGNDTTKPDLYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEQGRLLNTERG	61
DB	20	AAIPGNDVTTKPDLYLKNSQADISLALPPPEVGSILFLNDQAMYEKRLNTERG	79
QY	62	KLAAEDANLSSGVANAFSGAFSPITEKDAPLHLKLTNNIEDAGDLATRSADHYMRI	121
DB	80	EQAKADNADLAAAGVANAFSEAFGPIITEKDAPEIHLKLTNNIEDAGDLATRSADHYMRI	139
QY	122	RPFAFYGVSTNTTEODLKSNGSGYPSGHTSIGVATLVLAENIPORQNEILKGYELGQ	181
DB	140	RPFAFYGVATNTDQDLKSNGSGYPSGHTSIGVATLVLAENIPENDQKILKGYELGQ	199
QY	182	SRVTCGYHWSQDVDAARVYSAVATLTNPAPFOQLQKAAEPAQHOKK	230
DB	200	SRVTCGYHWSQDVDAARIVASGAVALTSHNPEFOKQAKADEPAKLKK	248

RESULT 2
S19187:
acid phosphatase (EC 3.1.3.2) - Morganella morganii
C:Species: Morganella morganii
C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 09-Jul-2004
C:Accession: S19187
R:Thaller, M.C.; Berluti, F.; Schippa, S.; Rosolini, G.M.
submitted to the EMBL Data Library, February 1992
A:Description: Sequencing the Morganella morganii phoC gene coding for a periplasmic ac
A:Reference number: S19187
A:Accession: S19187
A:Molecule type: DNA

A:Residues: 1-249 <THA>

A:Cross-references: UNIPROT:P28501; EMBL:X64444; NID:g44463; PIDN:CAA45774.1; PID:g44464
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic dc
C:Keywords: phosphoric monoester hydrolase
F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match

Best Local Similarity 81.4%; Score 969; DB 1; Length 249;
Matches 183; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 LALVATGNTTTPKPLLYLKNSDAINSLALPPPPVGSIAFLNDQAMYEQGRILNTER 60
DB 19 LLAIPAGNDATTPKPLLYLKNEQADISLKLPPPPVGSIGFLNDQAMYEGRILNTER 78
QY 61 GKLAEDANLSSGVANAFSGAFSPITEKDAAPLHKLTLMIEDAGLATRSKADHYMR 120
DB 79 GKQADADLAAGVATFSGAFSPITEKDSPELYKLTLMIEDADGLATRSKADHYMR 128
QY 121 IRPFAFVSTCTNTEQDKLSKNGSYPGHTSIGMATLVLAELINPORONEILKGYELG 180
DB 139 IRPFAFVSTCTNTEQDKLSKNGSYPGHTSIGMATLVLAELINPORONEILKGYELG 198
QY 181 QSRVIGYHMSDVAARVGSAAVATLHTNPAFOQLQAKAFPAHQK 231
DB 199 QSRVIGYHMSDVAARVGSAAVATLHTNPAFOQLQAKAFPAHQK 249

RESULT 3

A41330
acid phosphatase (EC 3.1.3.2) Phos precursor - Salmonella typhimurium
N:Alternate names: glycerophosphatase, nonspecific acid phosphatase; phosphomonoesterase
C:Species: Salmonella typhimurium
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S20958; A41330; S14515; S18926
R:Goidman, E.A.; Sater, J., M.H.; Ochman, H.
EMBL J. 11, 1309-1316, 1992

A:Title: Horizontal transfer of a phosphatase gene as evidence for mosaic structure of
A:Reference number: S20958; MUID:92224869; PMID:1339343
A:Accession: S20958
A:Molecule type: DNA
A:Residues: 1-250 <GRO>
A:Cross-references: UNIPROT:P26976; EMBL:X63539; NID:g47823; PIDN:CAA45144.1; PID:g47824
R:Kasahara, M.; Nakata, A.; Shingawa, H.
J. Bacteriol. 173, 6760-6765, 1991

A:Title: Molecular analysis of the Salmonella typhimurium phoA gene, which encodes nonsp
A:Reference number: A41330; MUID:92041557; PMID:1938882
A:Accession: A41330
A:Molecule type: DNA
A:Residues: 1-228 'SVRS' <KAS>
A:Cross-references: GB:X59036; NID:g48894; PIDN:CAA41760.1; PID:g48895
C:Genetics:

A:Gene: phoA
A:Map position: 96 min
A>Note: regulated by the two-component regulatory system consisting of phoP and phoQ
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic dc
C:Keywords: periplasmic space; phosphoric monoester hydrolase
F:108-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match
Best Local Similarity 40.8%; Score 485; DB 1; Length 250;
Matches 97; Conservative 29; Mismatches 76; Indels 0; Gaps 0;

QY 23 EAINSLALPPPPVGSIAFLNDQAMYEQGRILNTERGKLAEDANLSSGVANAFSGA 82
DB 31 EAVNSQYLPPLPPGNDPAFYVDEAFYKGYAIGSPRWMQAEEDADVSENIARLFSVP 90
QY 83 FGSPITEKDAAPLHKLTLMIEDAGLATRSKADHYMRIRPFAFVSTCTNTEQDKLSK 142
DB 91 VGAKINPKDPEPTNMMLKNLITMGYATATSAKKYTRRPVLFNHSICTRDEDTLTK 150
QY 143 NGSPSGHTSIGMATLVLAELINPORONEILKGYELGQSRVIGYHMSDVAARVGS 202
DB 151 NGSPSGHTSIGMATLVLAELINPORONEILKGYELGQSRVIGYHMSDVAARVGS 210

QY 203 AVATLHTNPAFOQLQAKAF 224
DB 211 VEFARLQITPAFOKSLAKVREE 232

RESULT 4

AF1025

acid phosphatase (EC 3.1.3.2) - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence revision 09-Nov-2001 #text_change 25-Aug-2003
C:Accession: AF1025

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Mole, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Farry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF1025

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09303.1; PID:g16505305; GSPDB:GN00176
C:Genetics:
A:Gene: phoA
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic d
C:Keywords: phosphoric monoester hydrolase

Query Match

Best Local Similarity 40.1%; Score 477; DB 2; Length 250;
Matches 95; Conservative 31; Mismatches 76; Indels 0; Gaps 0;

QY 23 EAINSLALPPPPVGSIAFLNDQAMYEQGRILNTERGKLAEDANLSSGVANAFSGA 82
DB 31 EAVNSQYLPPLPPGNDPAFYVDEAFYKGYAIGSPRWMQAEEDADVSENIARLFSVP 90
QY 83 FGSPITEKDAAPLHKLTLMIEDAGLATRSKADHYMRIRPFAFVSTCTNTEQDKLSK 142
DB 91 VGAKINPKDPEPTNMMLKNLITMGYATATSAKKYTRRPVLFNHSICTRDEDTLTK 150
QY 143 NGSPSGHTSIGMATLVLAELINPORONEILKGYELGQSRVIGYHMSDVAARVGS 202
DB 151 DSGPSGHTSIGMATLVLAELINPORONEILKGYELGQSRVIGYHMSDVAARVGS 210
QY 203 AVATLHTNPAFOQLQAKAF 224
DB 211 VEFARLQITPAFOKSLAKVREE 232

RESULT 5

A32044

acid phosphatase (EC 3.1.3.2) - Zymomonas mobilis
C:Species: Zymomonas mobilis
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A32044

R:Pond, J.L.; Eddy, C.K.; Mackenzie, K.F.; Conway, T.; Borecky, D.J.; Ingram, L.O.
J. Bacteriol. 171, 767-774, 1989
A:Title: Cloning, sequencing, and characterization of the principal acid phosphatase, th
A:Reference number: A32044; MUID:89123152; PMID:2914872
A:Accession: A32044

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <PON>
A:Cross-references: UNIPROT:P14924; GB:M24141; NID:g155613; PIDN:AAA27700.1; PID:g155614
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:99-212/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match

Best Local Similarity 27.6%; Score 329; DB 1; Length 264;
Matches 75; Conservative 37; Mismatches 97; Indels 4; Gaps 2;


```

QY 12 TKPDLYLKNSEAINSTALLPPPAVGS1AFUNDQAMEGRLRINTRECKLAABDANTS 71
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 33 SEPSTYHNSD---PLYLAPPTSGSPLOAHDDOTFNSTRQKSGSTRMALT1QDADLH 89
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 72 SGGVANAESPAGFSPITEKDAPALHKLITNMIEDADLATRSADHYMRIRPAFYGVST 131
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 90 LASVLKDVCAGAMNLDIAQLPLHLANTLKRALTERTYDIDGR-AKNMMNRKRPFVDTQPI 148
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 132 CNTTEODKLKSKGSPSGHTSIGMATVLAELNFORONEILKRGYELGSGRYICGYHWQ 191
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 149 CTKEKREBEGKCKGSPSGHTTIGWSVALTIAELIPHAANITLORGQIFGTSRIVCGAHWP 208
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 192 SDVDAARVYGSVAVALHTNTPAFCQOOLOKXKAE 224
   ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 209 SDVQAGYIMASGEITALLHGDADEFRRMELARKE 241
   ||| ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

```

RESULT 6
E87293
acid phosphatase [imported] - Caulobacter crescentus
C|Species: Caulobacter crescentus
C|Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 25-Aug-2003
C|Accession: E87293
R|Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heideberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolar
N. J.; Ermolaeva, M. J.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A|Title: Complete Genome Sequence of Caulobacter crescentus.
A|Reference number: A87249; MUID:21173698; PMID:11259647
A|Accession: E87293
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-258 <STD>
A|Cross-references: GB:AE005673; NID:gl3421511; PIDN:AAK22345.1; GSPDB:GN00148
C|Genetic(s)
A|Gene: CC0358
A|Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

	Query Match	Similarity	Score	DB 2	Length
Best Local	81	35.8%	Pred. No. 7.7e-17		258
Matches	81	Conservative	34	Mismatches	102
				Indels	9
				Gaps	8

```

RESULT 7
T286598
hypothetical protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 15-Oct-1999 #sequence_rev15-Oct-1999 #next_change 09-Jul-2004
C/Accession: T286598
R/Parkhill, J., Bentley, S.D., Barrell, B.G., Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A/Reference number: Z20512
A/Accession: T286598
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2314 <PAR>

```

[illegible]

RESULT 8

C63621

Probable acid phosphatase PA0190 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C|Species: *Pseudomonas aeruginosa*
C|Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 25-Aug-2003
C|Accession: C63621

R|Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Watterer, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,
J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A|Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
gen

A|Reference number: A62950; MUID:20437337; PMID:10984043

A|Accession: C63621

A|Status: preliminary

A|Molecule type: DNA

A|Residues: 1-241 <STO-
A|Cross-references: GB:AE004457; GB:AE004091; NID:g9946024; PIDN:AA03580.1; GSPDB:GN001
C|Genetics:
A|Experimental source: strain PA01

C|Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

A|Gene: PA0190

	Query Match	14.5%;	Score 172.5;	DB 2;	Length 241;
	Best Local Similarity	28.2%;	Pred. No. 8.1e-08;		
	Matches 58;	Conservative 34;	Mismatches 81;	Indels 33;	Gaps 8;
Cy	31 LPPPAVSIAFLNQAWYEGRLLENTER-CGLAEDA---NL--SSGGVANAFSGAFG 84				
Db	43 LPPPAADSAAAVADIGAVLEAQRLETPQVRVRVRRHDDQEDVNVFPFAGDILGASFDKER 102				
Cy	85 SPITEKDAPALHKLTLTMIEDAGDLATRSAKDHYMRIRPAFYGVSTCTTEQDK---L 140				
Db	103 LPLRTS---FFRRAGENVLE---VLMPAKKHFAPRPR-----EYTPKKVPVLP 146				
Cy	141 SKNGSYPSGHTSIGMATALVLAELNFORQNEILKRGELGCSRYTCGYHMOSDVDAARV 200				
Db	147 PEGESYPSGHTTDSYFKASILTMLVEHHDAFPARAEHQSRYVLACGVHPPSDLEGQTA 206				
Cy	201 GSAVATLHTNPAPFOQQLQKAKAEFA 226				
Db	207 AALVASTLADPA-----VAADFA 225				

RESULT 9
C96991
uncharacterized protein, containing probable phosphatase domain [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C96991
C;Mölling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183: 4823-4838, 2001
 A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
 A/Reference number: A96900; MUID:21359325; PMID:21359325
 A/Accession: C96991
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-591 <KUR>
 A/Cross-references: UNIPROT:097124; GB:AE001437; PIDN:AAK78718.1; PID:G15023624; GSPDB:G
 A/Experimental source: Clostridium acetobutylicum ATCC824
 A/Genetics:
 A/Map position: linear chromosome

Query Match 13.2%; Score 157; DB 2; Length 591;
 Best Local Similarity 25.7%; Pred. No. 6.4e-06;
 Matches 71; Conservative 37; Mismatches 100; Indels 68; Gaps 13;

QY 1 LALVATGNDTTKPLLY-LKNSKSAINSLALPP-PAVGSIA-FLNDQMYEQR 53
 DB 25 LKSNVNGEITSHAAVGVFVDEMKNNTNMSPSTNPAIGVSLKLMKPGISYDNGI 84
 QY 54 LRNT-----ERKTLAEDANTLS-----GGVANAFA--SCAFG 84
 DB 85 KLSNLIIMNTIQKVIQITVRRTSFOHQAYLDDRRNONSIVLDGLGYKDAFTKGA-G-143
 QY 85 SPIE---KDAPALHKLIT-----NKIEDAGDL-----ATRSAXDHY 119
 DB 144 TTITDIPKID--AINVOYTDKNAEGMAEESDLSGVVLTVDITNSASTPAPNYK 201
 QY 120 RIRPAPYG-VSTGNTEODKL---SKNGSPSGHTSIGMATAVLAENIPORONILR 175
 DB 202 YPRFMRSDKVKVPLTVPEKSTNPSDGGPFSHTNAATITDIALAVYVPERYQEMLTR 261
 QY 176 GYEIGQSRVTCGYHWSQVDPAARVGSAAVATLHTN 211
 DB 262 ASELGNDRIVAGMHSPLDIVIGRYMATAAASALNN 297

RESULT 10
 AB3118
 serine proteinase Atu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C/Species: Agrobacterium tumefaciens
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 A/Accession: AB3118
 R/Wood, D.W.; Seubul, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, B.W.
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB2577; MUID:21608550; PMID:11743193
 A/Accession: AB3118
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-660 <KUR>
 A/Cross-references: UNIPROT:08U788; GB:AE008689; PIDN:AA45360.1; PID:G17743054; GSPDB:G
 A/Experimental source: strain C58 (Dupont)
 A/Genetics:
 A/Map position: linear chromosome

Query Match 11.8%; Score 141; DB 2; Length 660;
 Best Local Similarity 33.0%; Pred. No. 0.00019;
 Matches 29; Conservative 20; Mismatches 33; Indels 6; Gaps 1;

QY 141 SKNGSPSGHTSIGMATAVLAENIPORONILKRGYELGQSRVTCGYHWSQVDPAARV 200
 DB 288 AKDGFSPSGHTNAAYLAIAVAVERFSELTLTAASELSESRIVAGMHSPLDIVIGRIT 347
 QY 201 GSAVATLHTNPAFQOOLQAKAEFAQH 228
 DB 348 ATMAAAMLODP-----KNAEYKKAH 369

RESULT 11
 E98169
 serine proteinase XF0267 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C/Species: Agrobacterium tumefaciens
 C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 A/Accession: E98169
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Kollan, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
 A/Reference number: A97359; MUID:21608551; PMID:11743194
 A/Accession: E98169
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-660 <KUR>
 A/Cross-references: UNIPROT:08U788; GB:AE007870; PIDN:AAK88879.1; PID:G15158646; GSPDB:G
 A/Genetics:
 A/Map position: linear chromosome

Query Match 11.8%; Score 141; DB 2; Length 660;
 Best Local Similarity 33.0%; Pred. No. 0.00019;
 Matches 29; Conservative 20; Mismatches 33; Indels 6; Gaps 1;

QY 141 SKNGSPSGHTSIGMATAVLAENIPORONILKRGYELGQSRVTCGYHWSQVDPAARV 200
 DB 288 AKDGFSPSGHTNAAYLAIAVAVERFSELTLTAASELSESRIVAGMHSPLDIVIGRIT 347
 QY 201 GSAVATLHTNPAFQOOLQAKAEFAQH 228
 DB 348 ATMAAAMLODP-----KNAEYKKAH 369

RESULT 12
 F75447
 vanadium chloroperoxidase-related protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 A/Accession: F75447
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: F75447
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-145 <WHI>
 A/Cross-references: UNIPROT:09RVL3; GB:AE001953; GB:AE000513; NID:G6458740; PIDN:AAFI058;
 A/Experimental source: strain R1
 A/Genetics:
 A/Map position: 1

Query Match 8.8%; Score 105; DB 2; Length 145;
 Best Local Similarity 37.5%; Pred. No. 0.041;
 Matches 24; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 145 SYPSGHTSIGMATAVLAENIPORONILKRGYELGQSRVTCGYHWSQVDPAARV 204
 DB 77 SYPSGHTVSGAAEVAIAQFFPLQARQLRRDADAFAFVVGSIHGVGVAGLVGQRY 136
 QY 205 VATL 208
 DB 137 ABAL 140

RESULT 13
 A87623
 PAP2 homolog protein [imported] - Caulobacter crescentus

C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: A87623
R/Nieman, M.C.; Feldlym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: A87623
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-259 <STO>
A/Cross-references: UNIPROT:Q9A424; GB:AE005673; NID:g13424659; PIDN:AAK24981.1; GSPDB:C
C/Genetics:
A/Gene: CC3019
C/Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom
Query Match 8.4%; Score 99.5; DB 2; Length 259;
Best Local Similarity 28.0%; Pred. No. 0.27;
Matches 47; Conservative 15; Mismatches 63; Indels 43; Gaps 5;
QY 70 LSSGVANAFSGAFSPITEKAPALHK-LITNMIED----- 106
DB 76 LRVGPALVGPFWLHVAADITLGSVAVLTLLILAFALGLSKRTWAMLALGAL 135
QY 107 -GDATRSAXDHVIRPFYGVSTCMTTBDKLSKNGSYPSGHTSIGMATLVL----- 161
DB 136 SGVTVSQGLKAVFGERDEARIVE-----AVNASFSGHAMSAVVFLTLGVLA 186
QY 162 AINFORNELLKRGY-----LGOSRVICGYHMQSDVDAAVVGSA 203
DB 187 ARFSRRRVKTLVSAVVVSLVGSASRYLGVHNVSDVLAGWSVGAA 234
RESULT 14
D82070
conserved hypothetical protein VC2488 (imported) - Vibrio cholerae (strain N16961 serogr
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: D82070
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charidson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H
L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: D82070
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-178 <HEI>
A/Cross-references: UNIPROT:Q9K85; GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAF9563
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2488
A/Map position: 1
C/Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom
Query Match 8.1%; Score 96; DB 2; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.34;
Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;
QY 115 KDHMRIRPFYGVSTCMTTBDKLSKNGSYPSGHTSIGMATLVLAEPQRONETLK 174
DB 81 KNSFQRRPQBSALVATVYITPSDRY---SLPSGHTAAAFVMTLIGIYIPHWYVALC 136
QY 175 RGEYIGOSRVICGYHMQSDVDAAVVG 201
DB 137 WAGLIGLARVLLGVHFLSDVITAGALG 163
RESULT 15
D87912

protein B0205.3 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: D87912
R/Anonymous: The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: D87912
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-608 <STO>
A/Cross-references: GB:chr_I; PIDN:AAK16991.1; PID:g3150473; GSPDB:GN00019; CESP:B0205.3
C/Genetics:
A/Gene: B0205.3
A/Map position: 1
Query Match 7.8%; Score 93; DB 2; Length 608;
Best Local Similarity 23.5%; Pred. No. 3.2;
Matches 42; Conservative 19; Mismatches 78; Indels 40; Gaps 5;
QY 66 EDANLSSGVANAFSGAFSPITEKAPALHKLITNMIEDAGLATRSAXDHVIRPFA 125
DB 456 EDGQAARFGGNGMDNFMGMV-ENDPDLALALRVSMEEBRARQAAAAAN----- 505
QY 126 FYGVSTCTTTTQDLSKNGSYPSGHTSIG-----WATLVLAEPQRONETLK 176
DB 506 -GGAAUSGADAEVAAAAVPLEMDMGAMTEQOLEWALRLSMQENAPAEQPV----- 559
QY 177 YELGOSRVICGYHMQSDVDAAVVGSAVVATLHTNPAPFOO-----LOKAKAEFAQHOKK 231
DB 560 -----QHEQMDVDGAPAVGDNVLDLMMNPILLQIYVDLPAANAEKDDKEX 607

Search completed: March 2, 2005, 20:27:45
Job time : 27.6667 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:06 ; Search time 114.745 Seconds
(without alignments)
1030.896 Million cell updates/sec

Title: US-09-807-990A-124

Perfect score: 1190

Sequence: 1 LALVATGNDTTTKPDLYLK.....PAFQOOLQKAEFAQHOKK 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1190	100.0	249	2	Q9S1A6
2	1095	92.0	248	2	Q9F1U0
3	1080	90.8	248	2	Q9R1U0
4	1065	88.5	248	2	Q9R1U6
5	1025	86.1	249	2	Q9S042
6	1022	85.9	249	2	Q9S099
7	986	82.9	248	1	PHON_PROST
8	969	81.4	249	1	PHOC_MORNO
9	772	64.9	263	2	O87188
10	582	48.9	246	2	Q9S035
11	577	48.5	246	2	Q9S909
12	576	48.4	246	2	Q931G8
13	571	48.0	246	2	O6XW11
14	510.5	42.9	280	2	O6AKP1
15	495.5	41.6	283	2	O6AKN1
16	485	40.8	250	1	PHON_SALTY
17	478	40.2	250	1	O8KR06
18	477	40.1	250	1	PHON_SALTY
19	477	40.1	250	1	O71EB8
20	464	39.0	285	2	O8BE10
21	433.5	36.4	280	2	O8B342
22	418.5	35.0	289	2	O7TU08
23	329	27.6	264	1	PPA_ZYMMO
24	274.5	23.1	258	2	O9AB73
25	220	18.5	231	2	O9B8U7
26	189.5	15.9	2314	2	O69822
27	187	15.7	423	2	O8E1D5
28	176.5	14.8	596	2	O6S6X3
29	172.5	14.5	241	2	O916U4
30	172	14.5	435	2	O6D5H8
31	157	13.2	591	2	O97124

32	153.5	12.9	643	2	O6FDK0	Q6fdk0 actinobact
33	149	12.5	986	2	O87U02	O87u02 pseudomonas
34	145.5	12.2	491	2	O6A6B5	O6a6b5 propionibac
35	144.5	12.1	128	2	O7TU17	O7tu17 prochloroco
36	144.5	12.1	657	2	O8Y350	O8y350 ralsionia s
37	143	12.0	622	2	O8NR65	O8nr65 corynebacte
38	142.5	12.0	115	2	O6ZXV7	O6zxv7 pseudomonas
39	142.5	12.0	115	2	O6ZXW1	O6zxw1 pseudomonas
40	141.5	11.9	115	2	O6ZXW2	O6zxw2 pseudomonas
41	141	11.8	660	2	O8U788	O8u788 agrobacteri
42	139.5	11.7	115	2	O6ZXV6	O6zxv6 pseudomonas
43	137.5	11.6	115	2	O6ZXV8	O6zxv8 pseudomonas
44	129.5	10.9	513	2	O8G856	O8g856 bifidobacte
45	108	9.1	260	2	O8E9E9	O8e9e9 shewanella

ALIGNMENTS

RESULT 1

ID	Q9S1A6	PRELIMINARY:	PRT:	249 AA.
AC	Q9S1A6			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Acid phosphatase (EC 3.1.3.2).			
GN	Name=pho;			
OS	Escherichia blattae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=563;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-UCM1650;			
RX	MEDLINE=20296667; PubMed=10835340; DOI=10.1093/emboj/19.11.2412;			
RA	Ishikawa K., Mihara Y., Gondoh K., Suzuki E., Asano Y.;			
RT	"X-ray structures of a novel acid phosphatase from Escherichia blattae			
RT	and its complex with the transition-state analog molybdate.";			
RL	EMBO J. 19:2412-2423 (2000).			
DR	EMBL; AB020481; BAA8942.1; .			
DR	PDB; 1D2T; X-ray; A/B/C=19-249.			
DR	PDB; 1I08; X-ray; A/D/E=19-249. B/C/F=-.			
DR	GO; GO:0030286; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA.			
DR	GO; GO:0003993; F:acid phosphatase activity; IEA.			
DR	GO; GO:0016787; F:hydrolase activity; IEA.			
DR	InterPro; IPR011158; Acid_Phase_C1Aa.			
DR	InterPro; IPR008934; AcPase_VanPase.			
DR	InterPro; IPR001011; Bac_AcPaseAa.			
DR	InterPro; IPR000326; Peptidase_PA_PTP.			
DR	Pfam; PF01569; PAP2; 1.			
DR	PIRSF; PIRSF000897; Acid_Phase_C1Aa; 1.			
DR	PRINTS; PRO0483; BACPHPTASE.			
DR	ProDom; PD009838; Bac_AcPaseAa; 1.			
DR	SMART; SM00014; acidPDC; 1.			
DR	PROSITE; PS01157; ACID_PHOSP_C1_A; 1.			
KW	Hydrolase.			
SC	SEQUENCE 249 AA; 26956 MW; 7A8A6CB61FC0CA3 CRC64;			
Query Match	100.0%; Score 1190; DB 2; Length 249;			
Best local similarity	100.0%; Pred. No. 1.8e-99;			
Matches 231; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 LALVATGNDTTTKPDLYLKNSAINSTALLPPPAVGSIATFLNDQMYEGGRLLRNTER 60			
Db	19 LALVATGNDTTTKPDLYLKNSAINSTALLPPPAVGSIATFLNDQMYEGGRLLRNTER 78			
Qy	61 GKLAEDANLSSGGVANAFAFGSPITTEKDAAPLHKLLTMTMDADGLATRSADKHMYR 120			
Db	79 GKLAEDANLSSGGVANAFAFGSPITTEKDAAPLHKLLTMTMDADGLATRSADKHMYR 138			
Qy	121 IRPAFYGVSTCTTEBDKLSKNGSPSGHTSIGMATALLVLAETNPORNEILLKRGVELG 180			

DB 139 IRPFAFYGVSTCNTTEODKLSKNGSYSGHISGMATLVLAELNPRQNEILKRGYELG 198
QY 181 OSRVICGYHMQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAFPAHQK 231
DB 199 OSRVICGYHMQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAFPAHQK 249

RESULT 2

Q9F1U1 PRELIMINARY; PRT; 248 AA.
AC O9F1U1; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acid phosphatase.
OS Name-pho;
OC Enterobacter aerogenes (aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_Taxid=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12010;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044338; BAB18917.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C1Aa.
DR InterPro; IPR008934; AcPase_VanPease.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Ptase_C1Aa; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
SQ SEQUENCE 248 AA; 26963 MW; 20EFA2C2E5EEB62D CRC64;

Query Match 92.0%; Score 1095; DB 2; Length 248;
Best Local Similarity 92.1%; Pred. No. 7, 1e-91;
Matches 211; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSAINSIALPPPAVGSIAFLNDQAMTEQRLIRTERG 61
DB 20 ALVPAAGNDATTKPDLYLKNAQALDSIALPPPEVGSIAFLNDQAMTEKRLIRTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPFAYGVSTCNTTEODKLSKNGSYSGHISGMATLVLAELNPRQNEILKRGYELG 181
DB 140 RPFAYGVSTCNTTEODKLSKNGSYSGHISGMATLVLAELNPRQNEILKRGYELG 199
QY 182 SRVICGYHMQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAFPAHQK 230
DB 200 SRVICGYHMQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAFPAHQK 248

RESULT 3

Q9F1U1 PRELIMINARY; PRT; 248 AA.
AC O9F1U1; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acid phosphatase.
OS Name-pho;
OC Enterobacter aerogenes (aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_Taxid=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12010;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044338; BAB18917.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C1Aa.
DR InterPro; IPR008934; AcPase_VanPease.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
SQ SEQUENCE 248 AA; 26963 MW; 20EFA2C2E5EEB62D CRC64;

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoulteilla.
OX NCBI_Taxid=575;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044345; BAB18918.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C1Aa.
DR InterPro; IPR008934; AcPase_VanPease.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Ptase_C1Aa; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
SQ SEQUENCE 248 AA; 26745 MW; 68F65CA2448BB3EF CRC64;

Query Match 90.8%; Score 1080; DB 2; Length 248;
Best Local Similarity 90.8%; Pred. No. 1, 6e-89;
Matches 208; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSAINSIALPPPAVGSIAFLNDQAMTEQRLIRTERG 61
DB 20 ALVPAAGNDATTKPDLYLKNAQALDSIALPPPEVGSIAFLNDQAMTEKRLIRTERG 79
QY 62 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 121
DB 80 KLAEDANLSSGGVANAFAFGSPITTEKDA PALHKLITNMIEDAGDLATRSADHYMRI 139
QY 122 RPFAYGVSTCNTTEODKLSKNGSYSGHISGMATLVLAELNPRQNEILKRGYELG 181
DB 140 RPFAYGVSTCNTTEODKLSKNGSYSGHISGMATLVLAELNPRQNEILKRGYELG 199
QY 182 SRVICGYHMQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAFPAHQK 230
DB 200 SRVICGYHMQSDVDAAARVGSAAVATLHTNPAFOOQLOKAKAFPAHQK 248

RESULT 4

Q9RLW6 PRELIMINARY; PRT; 248 AA.
AC Q9RLW6; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phoc protein precursor (BC 3.1.3.2).
OS Name-phoc;
GN Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_Taxid=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CGUG 225;
RA Pasariello C., Berlucchi F., Selan L., Thaller M.C., Rossolini G.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250377; CAB59725.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:hydrolyase activity; IEA.
DR InterPro; IPR011158; F:hydrolyase activity; IEA.
DR InterPro; IPR008934; AcPase_VanPease.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.

DR PIRSF, PIRSF000897; Acid Phase_ClaA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR Prodom; PD009838; Bac AcPaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 DR PROSITE; PS01157; ACID_PHOSP_CLA_A; 1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 248 Phoc.
 SQ SEQUENCE 248 AA; 27110 MW; ED6E9D8663636B0D CRC64;

Query Match 89.5%; Score 1065; DB 2; Length 248;
 Best Local Similarity 89.5%; Pred. No. 3.7e-88;
 Matches 205; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSEAINSLALPPPPAVGSAFLNDQAMYEQGLLNTERG 61
 DB 20 ALVPGNDVTTKPDLYLTNAQIDSLALPPPPAVGSAFLNDQAMYEQMTSVNTERG 79
 QY 62 KLAEDANLSSGGVANAFAFGSPITEKDAFALHKLITNIEDAGDLATRSADHYMRI 121
 DB 80 KLAEDANLSSGGVANAFAFGSPITEKDAFALHKLITNIEDAGDLATRSADHYMRI 139
 QY 122 RPAFYGVSTCNTTEODKLKNGSYPSGHTSIGMATLVLAIEINPORONEILKRGYELGQ 181
 DB 140 RPAFYGVSTCNTTEODKLKNGSYPSGHTSIGMATLVLAIEINPORONEILKRGYELG 199
 QY 182 SRVCGYMWQSDVDAARVGSAVVATLTNPAFOOOLOKAKAFPAHOXK 230
 DB 200 SRVCGYMWQSDVDAARVGSAVVATLTNPAFOOOLOKAKAFPAHOXK 248

RESULT 5

OS0542 PRELIMINARY; PRT; 249 AA.

AC OS0542;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Nonspecific phosphatase.
 GN Name=phon;
 OS Shigella flexneri.
 OG Plasmid pMYSH6000.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YSH6000;
 RX MEDLINE=96345620; PubMed=8755883;
 RA Uchiya K., Tobisuji M., Nikai T., Sugihara H., Sasakawa C.;
 RT "Identification and characterization of phon-Sf, a gene on the large
 RT plasmid of Shigella flexneri 2a encoding a nonspecific phosphatase.";
 RL J. Bacteriol. 178:4548-4554(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YSH6000;
 RA Uchiya K.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D82966; BAA11655.1; -.
 DR HSSP; Q9S1A6; 1D2T.
 DR GO; GO:0003288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR01158; Acid_Ptase_ClaA.
 DR InterPro; IPR00834; AcPase_VanPase.
 DR InterPro; IPR001011; Bac_AcPaseA.
 DR Pfam; PF01569; PAP2_1.
 DR PIRSF; PIRSF000897; Acid Phase_ClaA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR Prodom; PD009838; Bac_AcPaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 DR PROSITE; PS01157; ACID_PHOSP_CLA_A; 1.
 KW Plasmid.

SQ SEQUENCE 249 AA; 27177 MW; 58F34CEB034EB070 CRC64;
 Query Match: 86.1%; Score 1025; DB 2; Length 249;
 Best Local Similarity 84.8%; Pred. No. 1.6e-84;
 Matches 195; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 2 ALVATGNDTTKPDLYLKNSEAINSLALPPPPAVGSAFLNDQAMYEQGLLNTERG 61
 DB 20 ASIPGNDVTTKPDLYLTNDAIDSLALPPPGIGSAFLNDQAMYEKRLNTERG 79
 QY 62 KLAEDANLSSGGVANAFAFGSPITEKDAFALHKLITNIEDAGDLATRSADHYMRI 121
 DB 80 KLAEDANLSSGGVANAFAFGSPITEKDAFALHKLITNIEDAGDLATRSADHYMRI 139
 QY 122 RPAFYGVSTCNTTEODKLKNGSYPSGHTSIGMATLVLAIEINPORONEILKRGYELGQ 181
 DB 140 RPAFYGVSTCNTTEODKLKNGSYPSGHTSIGMATLVLAIEINPARODTLKRGYELG 199
 QY 182 SRVCGYMWQSDVDAARVGSAVVATLTNPAFOOOLOKAKAFPAHOXK 231
 DB 200 SRVCGYMWQSDVDAARVGSAVVATLTNPAFOOOLOKAKAFPAHOXK 249

RESULT 6

Q99099 PRELIMINARY; PRT; 249 AA.

AC Q99099; Q7BCK1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Phon1, periplasmic non specific acid ohosphatase (Phosphatase precursor).
 GN Name=phon1; Synonyms=phon-Sf;
 OS Shigella flexneri.
 OG Plasmid virulence plasmid pWR501, and Plasmid pCP301.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M90T;
 RX MEDLINE=20566792; PubMed=11115111;
 RA Buchrieser C., Glaeser P., Rusniok C., Nedjari H., d'Hauteville H.,
 RA Kunst F., Sansonetti P., Paros C.;
 RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
 RT by the type III secretion apparatus of Shigella flexneri.";
 RL Mol. Microbiol. 38:760-771(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID=virulence plasmid pWR501;
 RX MEDLINE=21189246; PubMed=11292750;
 RX DOI=10.1128/JAI.69.5.3271-3285.2001;
 RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
 RA Blatterner F.R.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid of
 RT Shigella flexneri.";
 RL Infect. Immun. 69:3271-3285(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=301 / Serotype 2a; PLASMID=PCP301;
 RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang D., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Kan B., Ding K., Chen S.,
 RA Chang H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 DR EMBL; AL381753; CAC05839.1; -.
 DR EMBL; AF348706; AAK18512.1; -.
 DR EMBL; AF386526; AAL72311.1; -.
 DR HSSP; Q9S1A6; 1D2T.

DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO: GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro: IPR01158; Acid_Phase_C1aA.
 DR InterPro: IPR008934; AcPase_VanPerase.
 DR InterPro: IPR001011; Bac_AcPaseA.
 DR InterPro: IPR003026; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Phase_C1aA_1.
 DR PRINTS: PR00483; BACPHTASE.
 DR ProDom: PD009838; Bac_AcPaseA_1.
 DR SMART: SM0014; acidPpc; 1.
 DR SMART: SM0014; acidPpc; 1.
 DR PROSITE: PS0157; ACID_PHOSP_C1_A; 1.
 DR Complete proteome; Plasmid.
 KW SEQUENCE 249 AA; 27211 MW; 9051C6C1CCE21ABA CRC64;

Query Match 85.9%; Score 1022; DB 2; Length 249;
 Best Local Similarity 86.2%; Pred. No. 2.9e-84;
 Matches 194; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 7 GNDVTTKPDLYLKNSSEAINSLALPPPPAVGSIAFLNDQAMYEQGRLLNTERG 66
 DB 25 GNDVTTKPDLYLKNSSEAINSLALPPPPAVGSIAFLNDQAMYEQGRLLNTERG 66
 QY 67 DANLSSGGVANAFAFGSPITTEKDAPELHKLITNMTEDAGDLATRSKDHVRIIPFAF 126
 DB 85 DANLSSGGVANAFAFGSPITTEKDAPELHKLITNMTEDAGDLATRSKDHVRIIPFAF 144
 QY 127 YGVSTCNTTEODKLSKNGSPSGHTSIGMATATLAFINPORONEILKRGYEIGQ 186
 DB 145 YGVSTCNTTEODKLSKNGSPSGHTSIGMATATLAFINPORONEILKRGYEIGQ 186
 QY 187 GYHWSQDVDAARIVASAVATLTNPAFQOOLKAKAEFAHQK 231
 DB 205 GYHWSQDVDAARIVASAVATLTNPAFQOOLKAKAEFAHQK 249

RESULT 7

PHOC_PROST STANDARD; PRT; 248 AA.
 AC P26975;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
 GN Name-phoc;
 OS Providencia stuartii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Providencia.
 OX NCBI_TaxID=588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PV81;
 RA Riccio M.L., Lombardi G., Chiesurin A., Satta G.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 or send an email to license@lsb-sib.ch).

DR EMBL: X64820; CAA46032.1; -;
 DR PIR: S19888; PAOFC3.
 DR HSSP: Q9S1A6; 1D2T.
 DR InterPro: IPR01158; Acid_Phase_C1aA.
 DR InterPro: IPR008934; AcPase_VanPerase.

DR InterPro: IPR001011; Bac_AcPaseA.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Phase_C1aA_1.
 DR PRINTS: PR00483; BACPHTASE.
 DR ProDom: PD009838; Bac_AcPaseA_1.
 DR SMART: SM0014; acidPpc; 1.
 DR PROSITE: PS0157; ACID_PHOSP_C1_A; 1.
 DR Hydrolase; Periplasmic; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 248
 SQ SEQUENCE 248 AA; 27043 MW; 2122A4B95E767CB2 CRC64;

Query Match 82.9%; Score 986; DB 1; Length 248;
 Best Local Similarity 81.2%; Pred. No. 5.3e-81;
 Matches 186; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 2 ALVANGNTTTPDLYLKNSSEAINSLALPPPPAVGSIAFLNDQAMYEQGRLLNTERG 61
 DB 20 ALVANGNTTTPDLYLKNSSEAINSLALPPPPAVGSIAFLNDQAMYEQGRLLNTERG 79
 QY 62 KLAEDANLSSGGVANAFAFGSPITTEKDAPELHKLITNMTEDAGDLATRSKDHVRI 121
 DB 80 KLAEDANLSSGGVANAFAFGSPITTEKDAPELHKLITNMTEDAGDLATRSKDHVRI 139
 QY 122 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATATLAFINPORONEILKRGYEIGQ 181
 DB 140 RPPAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATATLAFINPORONEILKRGYEIGQ 199
 QY 182 SRVICYHWSQDVDAARIVASAVATLTNPAFQOOLKAKAEFAHQK 230
 DB 200 SRVICYHWSQDVDAARIVASAVATLTNPAFQOOLKAKAEFAHQK 248

RESULT 8

PHOC_MORMO STANDARD; PRT; 249 AA.
 AC P28581;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Major phosphate-irrepressible acid phosphatase precursor (EC 3.1.3.2)
 GN Name-phoc;
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.
 RC STRAIN=RS12;
 RA MEDLINE=94362901; PubMed=8081499;
 RL Thaller M.C., Berlutti F., Schippa S., Lombardi G., Rosolini G.M.;
 CC "Characterization and sequence of Phoc, the principal phosphate-
 CC irrepressible acid phosphatase of Morganella morganii";
 CC Microbiology 140:1341-1350 (1994).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 10466;
 RX MEDLINE=20336426; PubMed=10877772;
 RA DOI=10.1128/AEM.66.7.2811-2816.2000;
 RL Mihara Y., Utagawa T., Yamada H., Asano Y.;
 CC "Phosphorylation of nucleosides by the mutated acid phosphatase from
 CC Morganella morganii";
 CC Appl. Environ. Microbiol. 66:2811-2816 (2000).
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- MISCELLANEOUS: Has a pH optimum around 6.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; X64444; CAA45774.1; -
 DR EMBL; AB035805; BAA96744.1; -
 DR PIR; S19187; S19187.
 DR HSSP; Q9S1A6; 1D2T.
 DR InterPro; IPR011158; Acid Phase ClsA.
 DR InterPro; IPR008934; AcPase VanPase.
 DR InterPro; IPR010111; Bac AcPaseA.
 DR InterPro; IPR000326; Peesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF00897; Acid_Pease_ClsA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac AcPaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
 DR Direct protein sequencing; Hydrolase; Periplasmic; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 249 Major phosphate-irrepressible acid
 FT phosphate.
 SQ SEQUENCE 249 AA; 26998 MW; C43F3698052B6A5C CRC64;
 Query Match 81.4%; Score 969; DB 1; Length 249;
 Best Local Similarity 79.2%; Pred. No. 1.9e-79;
 Matches 183; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 LALVATGDDTTKPLLYLKNSKSEAINSLALPPPPAVGSIAPLNDQMYEGRLNTERGKLAADA 60
 DB 19 LALPAGADATTTPLYLKNEQALDLSKLPPEVGSIQFLNDQMYEKRMILNTER 78
 QY 61 GKLAEDNANLSSGVANAFSGAFSPITEKDALPKLTLNMIEDAGDLATRSKDHMYR 120
 DB 79 GKQADADADLAAGVATAFSGAFSPITEKDSPELYKLTLMIEDAGDLATSAEHMYR 138
 QY 121 IRPFAVSTCNTNTTQDKLSKNGSPSGHTSIGMATLVLAELNPNQONETLKGYELG 180
 DB 139 IRPFAVSTCNTNTTQDKLSKNGSPSGHTSIGMATLVLAELNPNQONETLKGYELG 198
 QY 181 QSRVTCGYHMOVDVAAVGVAVATLTHTNPAFQOQLAKAKAFPHOKK 231
 DB 199 QSRVTCGYHMOVDVAAVGVAVATLTHTNPAFQOQLAKAKAFPHOKK 249

RESULT 9
 O87188 PRELIMINARY; PRT; 263 AA.
 AC O87188;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Acid phosphatase (PACP) precursor.
 GN Name=Phoc;
 OS Prevotella intermedia.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Prevotellaceae; Prevotella.
 OX NCBI_TaxID=26131;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25611;
 RX MEDLINE=20026825; PubMed=10559178;
 RA Chen X., Ansat T., Awano S., Iida T., Barik S., Takehara T.;
 RT "Isolation, cloning, and expression of an acid phosphatase containing
 RT phosphotyrosyl phosphatase activity from Prevotella intermedia.";
 RL J. Bacteriol. 181:7107-7114 (1999).
 DR EMBL; AB017537; BAA33148.1; -
 DR HSSP; Q9S1A6; 1D2T.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.

DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR011158; Acid Phase ClsA.
 DR InterPro; IPR008934; AcPase VanPase.
 DR InterPro; IPR010111; Bac AcPaseA.
 DR InterPro; IPR000326; Peesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF00897; Acid_Pease_ClsA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac AcPaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
 DR Signal.
 FT SIGNAL 1 20 Potential.
 SQ SEQUENCE 263 AA; 29201 MW; 6AD1C4A6470BF313 CRC64;
 Query Match 64.9%; Score 772; DB 2; Length 263;
 Best Local Similarity 65.9%; Pred. No. 1.4e-61;
 Matches 147; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 9 DTTKPDLYLYKNSKSEAINSLALPPPPAVGSIAPLNDQMYEGRLNTERGKLAADA 68
 DB 29 DARTPDLIYIQDQQTSSLELPPPPGSIQFLYDANQYQMGQMQRTRGDQAVADA 88
 QY 69 NLSGGVANAFSGAFSPITEKDALPKLTLNMIEDAGDLATRSKDHMYRIRPFAFG 128
 DB 89 RVGGDGVNAPFSEAFGIRKISKETPEIKYLVNMRDAGDLATRSKDHMYRVFPFAFN 148
 QY 129 VSTCNTTQDKLSKNGSPSGHTSIGMATLVLAELNPNQONETLKGYELGQSRVTCGY 188
 DB 149 EMTCTNPEQQLSTNGSPSGHTSIGMATLVLAELNPNQONETLKGYELGQSRVTCGY 208
 QY 189 HMOSVDAAVGVAVATLTHTNPAFQOQLAKAKAFPHOKK 231
 DB 209 HMOSVDAAVGVAVATLTHTNPAFQOQLAKAKAFPHOKK 251

RESULT 10
 O990G5 PRELIMINARY; PRT; 246 AA.
 AC O990G5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Phn2 (Apy), periplasmic phosphatase, apyrase, ATP diphosphohydrolase
 DE (Apyrase).
 GN Name=phn2 (apy); Synonym=S0004;
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M90T;
 RX MEDLINE=20566792; PubMed=1115111;
 RA Buchrieser C., Glaeser P., Ruesink C., Nedjari H., d'Hauteville H.,
 RA Kunst F., Sansonetti P., Parosot C.,
 RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
 RT by the type III secretion apparatus of Shigella flexneri.";
 RL Mol. Microbiol. 38:760-771 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID=virulence plasmid pWR501;
 RX MEDLINE=21189246; PubMed=11292750;
 RX DOI=10.1128/JAI.69.5.3271-3285.2001;
 RA Verketesan M.M., Goldberg M.B., Rose D.J., Grobeck B.J., Burland V.,
 RA Blatner F.R.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid of
 RT Shigella flexneri.";
 RL Infect. Immun. 69:3271-3285 (2001).
 DR EMBL; AL391753; CAC05771.1; -
 DR EMBL; AF348706; AAK18315.1; -
 DR HSSP; Q9S1A6; 1I1W8.

DB 205 IVCNHNHOSDVMMGRIMGAAVAVRLHADPAFLAEIEVAKELKAPRK 252

RESULT 15

06AKN1 PRELIMINARY; PRT; 283 AA.
 AC 06AKN1, 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Probable acid phosphatase.
 GN OrderedLocustNames=Dp2385;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 CC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LSY54 / DSM 12343;
 RX PubMed=15305914;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,
 BA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Glockner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902 (2004).
 RI EMBL; CR52870; CAG37094.1;
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR011158; F:acid phosphatase activity; IEA.
 DR InterPro; IPR008934; AcPase VanFerase.
 DR InterPro; IPR001011; Bac_AcPaseA.
 DR InterPro; IPR000326; Pesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid_Pase_C1sa; 1.
 DR PRINTS; PR00483; BACPMPHASE.
 DR PRODOM; PD009838; BACPMPHASE; 1.
 DR SMART; SM00014; acidPfc; 1.
 KW Complete proteome.
 SQ SEQUENCE 283 AA; 30483 MW; 86DD9AEED704D632 CRC64;

Query Match 41.6%; Score 495.5; DB 2; Length 283;
 Best Local Similarity 48.8%; Pred. No. 1,7e-36;

Matches 101; Conservative 30; Mismatches 75; Indels 1; Gaps 1;

QY 18 YLKSEAINSLALLPPPPVGSIAFLNDQAMTEQGRLRNTERGKLAEDANLSSGGVAN 77
 DB 43 YLPVDMLEPNSLTLLPPPPAEGSTAFALDREVNRQSHALQGTARWNLAKRDARLKFPQAAE 102
 QY 78 AFSGAFGSPITEKDPALHKLITNMIEDAGDLATSAKDHMRIRPPAFYGVSTCNTTEQ 137
 DB 103 TFSGALGIPISAEETPHLYMLRLRTIDA-ILSTYKANHRRTRPPFLNGETPTCTPKE 161
 QY 138 DKLKNGSYPSGHTSIGWATLVLAELNPNORNEILKRGYELGOSRVICGYHOSVDAA 197
 DB 162 AHMKSSGSPFSGHTSIGWAMALLIVEVAPFEQTDAILAGWAFGOSRIICNVHNSVDLMG 221
 QY 198 RVGSAVAVATLHTNPAFQOOLOKAAE 224
 DB 222 QVMGAAAVAKLHSDPAFLAEIEAAAE 248

Search completed: March 2, 2005, 20:26:48
 Job time : 117.745 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:12:01 ; Search time 116.732 Seconds
(without alignments)
755.417 Million cell updates/sec

Title: US-09-807-990A-125

Perfect score: 1173
Sequence: 1 LVPAGNDATTKEDLYLKNA.....NPAFOQLQKAKDEPAKTQK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq16Dec04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173	100.0	248	AAW06458	AAW06458 Enterobac
2	1173	100.0	248	AAW71031	AAW71031 Acid phos
3	1139	97.1	253	ABO61416	ABO61416 Klebsiell
4	1136	96.8	248	AAW06459	AAW06459 Klebsiell
5	1136	96.8	248	AAW71032	AAW71032 Acid phos
6	1127	96.1	248	AAW75068	AAW75068 Enterobac
7	1091	93.0	249	AAW06463	AAW06463 Escherich
8	1091	93.0	249	AAW71029	AAW71029 Acid phos
9	1091	93.0	249	AAW75064	AAW75064 Escherich
10	1084	92.4	231	AAW71034	AAW71034 Mutant ac
11	1079	92.0	231	AAW71035	AAW71035 Mutant ac
12	1062	90.5	231	AAW71036	AAW71036 Mutant ac
13	1056	90.0	231	AAW71037	AAW71037 Mutant ac
14	1053	89.8	231	AAW71038	AAW71038 Mutant ac
15	1051	89.6	231	AAW71040	AAW71040 Mutant ac
16	1051	89.6	231	AAW71042	AAW71042 Mutant ac
17	1048	89.3	231	AAW71039	AAW71039 Mutant ac
18	1047	89.3	231	AAW71041	AAW71041 Mutant ac
19	1035	88.2	248	AAW06457	AAW06457 Providenc
20	1035	88.2	248	AAW71030	AAW71030 Acid phos
21	983.5	83.8	249	AAW06462	AAW06462 Morganell
22	983.5	83.8	249	AAW71028	AAW71028 Acid phos
23	983.5	83.8	249	AAW75065	AAW75065 Morganell
24	983.5	83.8	249	AAW27583	AAW27583 Fusion pr
25	772	65.8	244	AAW06460	AAW06460 Serratia

26	772	65.8	244	2	AAW71033	AAW71033 Acid phos
27	574.5	49.0	246	2	AAW54082	AAW54082 Virulence
28	569.5	48.6	246	2	AAW35759	AAW35759 Apyrase (
29	475	40.5	232	4	AAW75066	AAW75066 Salmonell
30	341.5	29.1	264	4	AAW75067	AAW75067 Zymomonas
31	317	27.0	252	2	AAW20014	AAW20014 Ascorbic
32	193.5	16.5	943	8	ADL05772	ADL05772 M. catarr
33	191.5	16.3	428	7	ABO64424	ABO64424 Klebsiell
34	166	14.2	253	7	ABO79811	ABO79811 Pseudomon
35	165	14.1	585	8	ADG32050	ADG32050 Mutant B-
36	165	14.1	594	8	ADG32068	ADG32068 Mutant B
37	153	13.0	987	7	ADP07500	ADP07500 Bacteri
38	149.5	12.7	508	4	AAW56365	AAW56365 Propionib
39	149.5	12.7	508	6	ABW52884	ABW52884 Propionib
40	135	11.5	513	5	ABP65275	ABP65275 Bifidobac
41	133	11.3	622	4	AAW91063	AAW91063 C. glutami
42	133	11.3	622	7	ADJ87369	ADJ87369 DNA repli
43	106.5	9.1	201	7	ADM26585	ADM26585 Hyperther
44	105	9.0	58	5	ABP08795	ABP08795 Human ORF
45	96	8.2	178	6	ABU49566	ABU49566 Protein e

ALIGNMENTS

RESULT 1	AAW06458	standard; protein; 248 AA.
ID	AAW06458	standard; protein; 248 AA.
AC	AAW06458;	
XX		
DT	13-AUG-1997	(first entry)
XX		
DE	Enterobacter aerogenes IFO 12010 acid phosphatase.	
XX		
KW	IFO 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester; condiment; pharmaceutical; intermediate.	
XX		
OS	Enterobacter aerogenes.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 92	/note= "optionally replaced by another amino acid"
FT	Misc-difference 171	/note= "optionally replaced by another amino acid"
FT	Misc-difference 171	/note= "optionally replaced by another amino acid"
XX		
PN	WO9637603-A1.	
XX		
PD	28-NOV-1996.	
XX		
PF	24-MAY-1996;	96WO-JP001402.
XX		
PR	25-MAY-1995;	95JP-00149781.
XX		
PR	26-MAR-1996;	96JP-00094680.
XX		
PA	(AJIN) AJINOMOTO CO INC.	
XX		
PI	Mihara Y, Uragawa T, Yamada H, Asano Y;	
XX		
DR	WPI; 1997-021215/02.	
XX		
DR	N-PEDB; AAT45007.	
XX		
PT	Efficient production of nucleoside 5'-phosphate - by reaction of a nucleoside with a phosphoric acid donor in the presence of an acid phosphatase.	
XX		
PS	Claim 3; Page 67-68; 95pp; Japanese.	
XX		
CC	The present sequence is the Enterobacter aerogenes IFO 12010 acid phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate ester from the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5. The PA can be used for the economic and efficient production	

CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
 CC and intermediates for pharmaceuticals
 XX
 SQ Sequence 248 AA;

Query Match 100.0%; Score 1173; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.5e-118;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
 DB 21 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
 QY 61 LAADANLSAGVANAFASSAFSGSPITEKAPQHLKLTNMIEDAGDLATRSAXEKYMRIR 120
 DB 81 LAADANLSAGVANAFASSAFSGSPITEKAPQHLKLTNMIEDAGDLATRSAXEKYMRIR 140
 QY 121 PFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQKONEILKRGYELGES 180
 DB 141 PFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQKONEILKRGYELGES 200
 QY 181 RVICGTHWQSDVDARIVGSAAVATLTNPAPFOOOLQAKDEFKATOK 228
 DB 201 RVICGTHWQSDVDARIVGSAAVATLTNPAPFOOOLQAKDEFKATOK 248

RESULT 2

AAW71031
 ID AAW71031 standard; protein; 248 AA.

AC AAW71031;
 DT 21-OCT-1998. (first entry)

DE Acid phosphatase enzyme amino acid sequence.
 KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KM intermediate.
 OS Enterobacter aerogenes.

FN EP857788-A2.
 PD 12-AUG-1998.

PF 20-NOV-1997; 97EP-00309365.
 PR 21-NOV-1996; 96UP-00311103.
 XX 18-JUN-1997; 97JP-00161674.

PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;
 DR WPI; 1998-416010/36.
 DR N-PSDB; AAW43060.

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 with phosphate donor in presence of acid phosphatase - used as seasonings
 or pharmaceutical intermediates.

PS Example 23; Page 44; 83pp; English.

CC The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them

SQ Sequence 248 AA;

Query Match 100.0%; Score 1173; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.5e-118;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
 DB 21 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
 QY 61 LAADANLSAGVANAFASSAFSGSPITEKAPQHLKLTNMIEDAGDLATRSAXEKYMRIR 120
 DB 81 LAADANLSAGVANAFASSAFSGSPITEKAPQHLKLTNMIEDAGDLATRSAXEKYMRIR 140
 QY 121 PFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQKONEILKRGYELGES 180
 DB 141 PFAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPQKONEILKRGYELGES 200
 QY 181 RVICGTHWQSDVDARIVGSAAVATLTNPAPFOOOLQAKDEFKATOK 228
 DB 201 RVICGTHWQSDVDARIVGSAAVATLTNPAPFOOOLQAKDEFKATOK 248

RESULT 3

ABO61416
 ID ABO61416 standard; protein; 253 AA.

AC ABO61416;

DT 29-JUL-2004 (first entry)

DE Klebsiella pneumoniae polypeptide seqid 7933.

KW Recombinant expression vector; transcription regulatory element;
 KM Klebsiella pneumoniae protein; antibacterial; vaccine.

OS Klebsiella pneumoniae.

FN US610836-B1.

PD 26-AUG-2003.

PF 27-JAN-2000; 2000US-00489039.

PR 29-JAN-1999; 99US-0117747P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Breton GL, Osborne M;

DR WPI; 2003-895346/82.

DR N-PSDB; ACH94967.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 preparing a vaccine composition against Klebsiella pneumoniae.

PS Disclosure; SEQ ID NO 7933; 932pp; English.

CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention

SQ Sequence 253 AA;

Query Match 97.1%; Score 1139; DB 7; Length 253;
 Best Local Similarity 96.9%; Pred. No. 7.9e-115;
 Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60

Best Local Similarity 96.9%; Pred. No. 1,66-114;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
Db 21 LVPAAGNDATTKPDLYYLKNAQAIDSLLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
QY 61 LAAEDANLSAGVANAFAFSAPFSPTTEKDA POLHKLITNMI EDAGDLATRSAREKYMIR 120
Db 81 LAAEDANLSAGVANAFAFSAPFSPTTEKDA POLHKLITNMI EDAGDLATRSAREKYMIR 140
QY 121 PPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIGES 180
Db 141 PPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIGES 200
QY 181 RVICGYHMOSDVAARIIVGSAVVATLTNPAFOOOLQAKDEFAKTOK 228
Db 201 RVICGYHMOSDVAARIIVGSAVVATLTNPAFOOOLQAKDEFAKTOK 248

RESULT 6

AAB75068
ID AAB75068 standard; protein; 248 AA.

AC AAB75068;

DT 23-JUL-2001 (first entry)

DE Enterobacter aerogenes nucleotide-5'-phosphate producing enzyme protein.

KM Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
KM transphosphorylation; phosphatase; protein co-ordinate data;
KM X-ray structural analysis; three-dimensional structure.

OS Enterobacter aerogenes.

PN WO200118184-A1.

PD 15-MAR-2001.

PF 01-SEP-2000; 2000WO-JP005973.

PR 03-SEP-1999; 99JP-00249545.

PA (AJIN) AJINOMOTO CO INC.

PI Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H,
PI Kurahashi O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;

DR WPI; 2001-380914/40.
DR N-PSDB; AAH19705.

PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing
PT activity and having a specific three-dimensional structure for production
PT of nucleosides as pharmaceutical intermediates.

PS Example 19; Page 117-118; 150pp; Japanese.

CC The present invention describes a variant nucleoside-5'-phosphate
CC producing enzyme which is a modification of a transphosphorylase or
CC phosphatase which contains a lysine, two arginine and two histidine
CC residues and in which the C-alpha distances between these residues are
CC enclosing a space which permits the binding of a nucleoside with these
CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
CC expression vectors containing the DNA; (3) host cells transformed by the
CC vectors; (4) preparation of the variant enzyme by culture of the
CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
CC or transphosphorylase using the structural coordinates derived from the
CC enzyme. The variant enzymes with increased efficiency for production of
CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
CC AAH19701 to AAH19785 and AAB75064 to AAB75101 represent sequences used in
CC the exemplification of the present invention

XX SQ Sequence 248 AA;

Query Match 96.1%; Score 1127; DB 4; Length 248;
Best Local Similarity 96.1%; Pred. No. 1,66-113;
Matches 219; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTKPDLYYLKNAQAIDSLLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
Db 21 LVPAAGNDATTKPDLYYLKNAQAIDSLLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 80
QY 61 LAAEDANLSAGVANAFAFSAPFSPTTEKDA POLHKLITNMI EDAGDLATRSAREKYMIR 120
Db 81 OAOADADLAAGVANAFAFSAPFSPTTEKDA POLHKLITNMI EDAGDLATRSAREKYMIR 140
QY 121 PPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIGES 180
Db 141 PPAFYGVSTCNTTKDDKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYEIGES 200
QY 181 RVICGYHMOSDVAARIIVGSAVVATLTNPAFOOOLQAKDEFAKTOK 228
Db 201 RVICGYHMOSDVAARIIVGSAVVATLTNPAFOOOLQAKDEFAKTOK 248

RESULT 7

AAW06463
ID AAW06463 standard; protein; 249 AA.

AC AAW06463;

DT 13-AUG-1997 (first entry)

DE Escherichia blattae JCM 1650 acid phosphatase.

KM JCM 1650; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KM condiment; pharmaceutical; intermediate.

OS Escherichia blattae.

PH Key Location/Qualifiers
FT Peptide 1..18
FT Peptide /label= sig_peptide
FT Peptide 19..249
FT /label= mat_peptide

FT Misc-difference 92
FT /note= "optionally replaced by another amino acid"
FT Misc-difference 171
FT /note= "optionally replaced by another amino acid"

XX WO9637603-A1.
XX 28-NOV-1996.
XX PD 24-MAY-1996; 96WO-JP001402.
XX PF 25-MAY-1995; 95JP-00149781.
XX PR 26-MAR-1996; 96JP-00094680.
XX PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;
PI WPI; 1997-021215/02.
DR N-PSDB; AAT45011.

PT Efficient production of nucleoside 5'-phosphate - by reaction of a
PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphatase.

PS Claim 3; Page 56-58; 95pp; Japanese.

CC The present sequence is the Escherichia blattae JCM 1650 acid phosphatase
CC (AP), which can be used to produce a nucleoside 5'-phosphate ester from

CC the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl-
CC or carboxy-1-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5.
CC The PA can be used for the economic and efficient production of
CC nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and
CC intermediates for pharmaceuticals

XX Sequence 249 AA;

SO Query Match 93.0%; Score 1091; DB 2; Length 249;

Best Local Similarity 92.1%; Pred. No. 1.3e-109; Indels 0; Gaps 0;

Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTPKEDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
DB 21 LVATGNDTTPKEDLYLKNQSEAINSLALPPPAVGSIAFLNDQAMYEKGRLLRTERGK 80
QY 61 LAEDANLSAGGVANAFSGAFSGPTEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 120
DB 81 LAEDANLSAGGVANAFSGAFSGPTEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 140
QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGSS 180
DB 141 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGSS 200
QY 181 RVICGYHMQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 228
DB 201 RVICGYHMQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 248

RESULT 8

AAM71029 AAM71029 standard; protein; 249 AA.

XX AAM71029;

XX 21-OCT-1998 (first entry)

DE Acid phosphatase enzyme amino acid sequence.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KM intermediate.

XX Escherichia blattae.

OS Escherichia blattae.

XX Key Location/Qualifiers

FT Peptide 1..18
FT Protein /note= "signal peptide"
FT Protein 19..249
FT Protein /note= "mature protein; Claim 6"

XX EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97EP-00309365.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

XX N-PSDB; AAV43046.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.

XX Example 12; Page 35-36; 83pp; English.

XX The present sequence represents an acid phosphatase enzyme. The

CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate esters. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC that has been transformed with recombinant DNA containing a gene coding
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them

XX Sequence 249 AA;

SO Query Match 93.0%; Score 1091; DB 2; Length 249;

Best Local Similarity 92.1%; Pred. No. 1.3e-109; Indels 0; Gaps 0;

Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAAGNDATTPKEDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
DB 21 LVATGNDTTPKEDLYLKNQSEAINSLALPPPAVGSIAFLNDQAMYEKGRLLRTERGK 80
QY 61 LAEDANLSAGGVANAFSGAFSGPTEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 120
DB 81 LAEDANLSAGGVANAFSGAFSGPTEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 140
QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGSS 180
DB 141 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGSS 200
QY 181 RVICGYHMQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 228
DB 201 RVICGYHMQSDVDARIVGSAAVATLHTNPAFOOLQKAKDEFKATOK 248

RESULT 9

AAB75064 AAB75064 standard; protein; 249 AA.

XX AAB75064;

XX 23-JUN-2001 (first entry)

DE Escherichia blattae nucleoside-5'-phosphate producing enzyme protein.

XX Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
KM transphosphorylation; phosphate; protein co-ordinate data;

XX X-ray structural analysis; three-dimensional structure.

OS Escherichia blattae.

XX WO200118184-A1.

XX 15-MAR-2001.

XX 01-SEP-2000; 2000WO-JP005973.

XX 03-SEP-1999; 99JP-00249545.

XX (AJIN) AJINOMOTO CO INC.

XX Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;

XX Kurahashi O, Kouda T, Shimooka M, Kozutsu R, Asano Y;

XX WPI; 2001-380914/40.

XX N-PSDB; AAH19701.

XX Variant enzyme having elevated nucleoside 5'-prime phosphate producing
PT activity and having a specific three-dimensional structure for production
PT of nucleosides as pharmaceutical intermediates.

XX Disclosure; Page 107; 150pp; Japanese.

XX The present invention describes a variant nucleoside-5'-phosphate
CC producing enzyme which is a modification of a transphosphorylase or
CC phosphatase which contains a lysine, two arginine and two histidine

CC residues and in which the C-alpha distances between these residues are
 CC enclosing a space which permits the binding of a nucleoside with these
 CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
 CC expression vectors containing the DNA; (3) host cells transformed by the
 CC vectors; (4) preparation of the variant enzyme by culture of the
 CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
 CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
 CC or transphosphorylase using the structural coordinates derived from the
 CC enzyme. The variant enzymes can be used as pharmaceutical intermediates.
 CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
 CC AAH19701 to AAH19785 and AAB75064 to AAB75101 represent sequences used in
 CC the exemplification of the present invention

XX SQ Sequence 249 AA;

Query Match 93.0%; Score 1091; DB 4; Length 249;
 Best Local Similarity 92.1%; Pred. No. 1.3e-109;

Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAGNDATTTPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLNTERGK 60
 DB 21 LVATGNDTTTPDLYLKNSEAINSLALLPPPAVGSIAFLNDQAMYEQRLNTERGK 80
 QY 61 LAEDANLSAGVANAFAFGSPITEKDAFQHLKLTNNMEDAGDLATRSAREKYMIR 120
 DB 81 LAEDANLSAGVANAFAFGSPITEKDAFQHLKLTNNMEDAGDLATRSAREKYMIR 140
 QY 121 PFAFYGVSTCNTTEODKLKNGSYPSGHTSIGWATLVLAETNPORONEILKRGYELGES 180
 DB 141 PFAFYGVSTCNTTEODKLKNGSYPSGHTSIGWATLVLAETNPORONEILKRGYELGES 200
 QY 181 RVICGYHMOQSDVDAAIVGSAAVATLTNPAPFOQOLQKAKDEFKATOK 228
 DB 201 RVICGYHMOQSDVDAAIVGSAAVATLTNPAPFOQOLQKAKDEFKATOK 248

RESULT 10

AAW71034
 ID AAW71034 standard; protein; 231 AA.

XX AC AAW71034;

XX DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of *Escherichia blattae*.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 mutant; intermediate.

XX OS Synthetic.
 OS *Escherichia blattae*.

XX FH Key Location/Qualifiers

FT Misc-difference 74
 FT /label= G74D

XX PN EP857788-A2.

XX PD 12-AUG-1998.

XX PF 20-NOV-1997; 97EP-00309365.

XX PR 21-NOV-1996; 96GP-00311103.

XX PR 18-JUN-1997; 97JP-00161674.

XX PA (AJIN) AJINOMOTO CO INC.

XX PI Mihara Y, Utagawa T, Yamada H, Asano Y;

XX DR WPI; 1998-416010/36.

XX PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings

PT or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided

XX SQ Sequence 231 AA;

Query Match 92.4%; Score 1084; DB 2; Length 231;
 Best Local Similarity 91.7%; Pred. No. 6.6e-109;

Matches 209; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 LVPAGNDATTTPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLNTERGK 60
 DB 3 LVATGNDTTTPDLYLKNSEAINSLALLPPPAVGSIAFLNDQAMYEQRLNTERGK 62
 QY 61 LAEDANLSAGVANAFAFGSPITEKDAFQHLKLTNNMEDAGDLATRSAREKYMIR 120
 DB 63 LAEDANLSAGVANAFAFGSPITEKDAFQHLKLTNNMEDAGDLATRSAREKYMIR 122
 QY 121 PFAFYGVSTCNTTEODKLKNGSYPSGHTSIGWATLVLAETNPORONEILKRGYELGES 180
 DB 123 PFAFYGVSTCNTTEODKLKNGSYPSGHTSIGWATLVLAETNPORONEILKRGYELGES 182
 QY 181 RVICGYHMOQSDVDAAIVGSAAVATLTNPAPFOQOLQKAKDEFKATOK 228
 DB 183 RVICGYHMOQSDVDAAIVGSAAVATLTNPAPFOQOLQKAKDEFKATOK 230

RESULT 11

AAW71035
 ID AAW71035 standard; protein; 231 AA.

XX AC AAW71035;

XX DT 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of *Escherichia blattae*.

KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 mutant; intermediate.

XX OS Synthetic.
 OS *Escherichia blattae*.

XX FH Key Location/Qualifiers

FT Misc-difference 74
 FT /label= G74D

XX FT Misc-difference 153
 FT /label= I153T

XX PN EP857788-A2.

XX PD 12-AUG-1998.

XX PF 20-NOV-1997; 97EP-00309365.

XX PR 21-NOV-1996; 96GP-00311103.

XX PR 18-JUN-1997; 97JP-00161674.

XX PA (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;
 XX
 XX WPI, 1998-416010/36.
 XX
 PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 XX
 PS Example 19; Page; 83pp; English.
 XX
 CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 XX
 SQ Sequence 231 AA;
 Query Match 92.0%; Score 1079; DB 2; Length 231;
 Best Local Similarity 91.2%; Pred. No. 2.3e-108;
 Matches 208; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 LVPAGNDATTPKPDLYLLKNAQALDLSLALPPPEVGSIAFLNDQAMEYGRLLRNTERGK 60
 DB 3 LVATGNDTTTKPDLYLLKNSSEALNSLALPPPAVGSIAFLNDQAMEYGRLLRNTERGK 62
 QY 61 LAEDANISAGGVANAFSSAFSGSPITEKDAPOHLKLTMTMIDADGLATRSKKEKYMIR 120
 DB 63 LAEDANISAGGVANAFSGAFSGSPITEKDAPOHLKLTMTMIDADGLATRSKKEKYMIR 122
 QY 121 PFAFYGVSTCNTTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 180
 DB 123 PFAFYGVSTCNTTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 182
 QY 181 RVICGYHMQSDVDAAARIYGSAAVVATLHTNPAFOQLQAKKEFAQHOK 228
 DB 183 RVICGYHMQSDVDAAARIYGSAAVVATLHTNPAFOQLQAKKEFAQHOK 230
 RESULT 12
 AAW71036
 ID AAW71036 standard; protein; 231 AA.
 XX
 AC AAW71036;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Mutant acid phosphatase enzyme of Escherichia blattae.
 XX
 KM Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KM mutant; intermediate.
 XX
 OS Synthetic.
 OS Escherichia blattae.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 63
 FT Misc-difference /label= L63Q
 FT Misc-difference 65
 FT Misc-difference /label= A65Q
 FT Misc-difference 66
 FT Misc-difference /label= E66A
 FT Misc-difference 74
 FT Misc-difference /label= G74D
 FT Misc-difference 153
 FT /label= I153T

XX
 PN EP857788-A2.
 XX
 PD 12-AUG-1998.
 XX
 PF 20-NOV-1997; 97EP-00309365.
 XX
 PR 21-NOV-1996; 96JP-00311103.
 XX
 PR 18-JUN-1997; 97JP-00161674.
 XX
 PA (AJTN) AJINOMOTO CO INC.
 XX
 PI Mihara Y, Utagawa T, Yamada H, Asano Y;
 XX
 XX WPI, 1998-416010/36.
 XX
 PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 XX
 PS Example 19; Page; 83pp; English.
 XX
 CC AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 XX
 SQ Sequence 231 AA;
 Query Match 90.5%; Score 1062; DB 2; Length 231;
 Best Local Similarity 89.9%; Pred. No. 1.6e-106;
 Matches 205; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 1 LVPAGNDATTPKPDLYLLKNAQALDLSLALPPPEVGSIAFLNDQAMEYGRLLRNTERGK 60
 DB 3 LVATGNDTTTKPDLYLLKNSSEALNSLALPPPAVGSIAFLNDQAMEYGRLLRNTERGK 62
 QY 61 LAEDANISAGGVANAFSSAFSGSPITEKDAPOHLKLTMTMIDADGLATRSKKEKYMIR 120
 DB 63 QAADANISAGGVANAFSGAFSGSPITEKDAPOHLKLTMTMIDADGLATRSKKEKYMIR 122
 QY 121 PFAFYGVSTCNTTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 180
 DB 123 PFAFYGVSTCNTTTEBODKLSKNGSYPSGHTSIGMATALVLAETINPORONEILKRGYELGES 182
 QY 181 RVICGYHMQSDVDAAARIYGSAAVVATLHTNPAFOQLQAKKEFAQHOK 228
 DB 183 RVICGYHMQSDVDAAARIYGSAAVVATLHTNPAFOQLQAKKEFAQHOK 230
 RESULT 13
 AAW71037
 ID AAW71037 standard; protein; 231 AA.
 XX
 AC AAW71037;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Mutant acid phosphatase enzyme of Escherichia blattae.
 XX
 KM Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KM mutant; intermediate.
 XX
 OS Synthetic.
 OS Escherichia blattae.

```

XX Key Location/Qualifiers
FH Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= A66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 85 /label= S85Y
FT Misc-difference 153 /label= I153T
FT EP857788-A2.
XX 12-AUG-1998.
XX 20-NOV-1997; 97EP-00309365.
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX (AJTN ) AJINOMOTO CO INC.
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX Example 19; Page; 83pp; English.
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
XX Sequence 231 AA;

```

```

Query Match 90.0%; Score 1056; DB 2; Length 231;
Best Local Similarity 89.5%; Pred. No. 7.4e-106;
Matches 204; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
DB 1 LVAGNDATTKPLDYLYLKNQAIDSLALPPPEVGSIAFINDOAMYEKGRLLRTERGX 60
QY 1 LVAGNDATTKPLDYLYLKNQAIDSLALPPPEVGSIAFINDOAMYEKGRLLRTERGX 60
DB 3 LVATGNDYTKPLDYLYLKNSEALNSLALPPPAVGSIAFINDOAMYEKGRLLRTERGX 62
QY 61 LAEDANLISAGVANAFFSFAFGSPITEKAPOLHKLITNMIEDAGLATSANAKYRIR 120
DB 63 QAOADANLSSGDVANAFFSFAFGFPIREKAPALHKLITNMIEDAGLATSADHYRIR 122
QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHSIGWATLVLAETNPORONELKRGYLGSS 180
DB 123 PFAFYGVSTCNTTEODKLSKNGSPSGHSTGWATLVLAETNPORONELKRGYLGSS 182
QY 181 RVICGHWOSDVDAARVGSAAVATLHTNPAFOOOLQKADFEAKTOK 228
DB 183 RVICGHWOSDVDAARVGSAAVATLHTNPAFOOOLQKADFEAKTOK 230

```

RESULT 14

```

AAW71038
ID AAW71038 standard; protein; 231 AA.
XX
XX AAW71038;
XX 21-OCT-1998 (first entry)
XX Mutant acid phosphatase enzyme of Escherichia blattae.
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX mutant; intermediate.
XX Synthetic.
XX Escherichia blattae.
XX
XX Key Location/Qualifiers
FH Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= A66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 135 /label= T135K
FT Misc-difference 136 /label= E136D
FT Misc-difference 153 /label= I153T
FT EP857788-A2.
XX 12-AUG-1998.
XX 20-NOV-1997; 97EP-00309365.
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX (AJTN ) AJINOMOTO CO INC.
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX Example 19; Page; 83pp; English.
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
XX Sequence 231 AA;

```

```

Query Match 89.8%; Score 1053; DB 2; Length 231;
Best Local Similarity 89.0%; Pred. No. 1.6e-105;
Matches 203; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 1 LVAGNDATTKPLDYLYLKNQAIDSLALPPPEVGSIAFINDOAMYEKGRLLRTERGX 60

```

```

Db      3 LVATGNDTTTKPDLYLLKNSEAINSLALPPPPAVGSIAPFNDQAMYEQGRLLRNTTERGK 62
QY      61 LAEPDANLSAGVANAFFSAGFSPITTEKDAPOLHKLTLNMTEDAGDLATRSKEXMYRIR 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 QOQADANLSSGGVANAFFSAGFSPITTEKDAPOLHKLTLNMTEDAGDLATRSKEXMYRIR 122
QY      121 PFAFYGVSTCNTTTEODKLSKNGSYSPGHTSIGMATALVLAIEINPQRONEILKRGYELGES 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123 PFAFYGVSTCNTKDDKLSKNGSYSPGHTSIGMATALVLAIEINPQRONEILKRGYELGES 182
QY      181 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEPAKTOK 228
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      183 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEPAKTOK 230

RESULT 15
AAW71040
ID      AAW71040 standard; protein; 231 AA.
XX
AC      AAW71040;
XX
DT      21-OCT-1998 (first entry)
XX
DE      Mutant acid phosphatase enzyme of Escherichia blatae.
XX
KW      Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
        mutant; intermediate.
XX
OS      Synthetic.
XX
OS      Escherichia blatae.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 63      /label= L63Q
FT      Misc-difference 65      /label= A65Q
FT      Misc-difference 66      /label= E66A
FT      Misc-difference 69      /label= N69D
FT      Misc-difference 71      /label= S71A
FT      Misc-difference 72      /label= S72A
FT      Misc-difference 74      /label= G74D
FT      Misc-difference 116     /label= D116E
FT      Misc-difference 135     /label= T135K
FT      Misc-difference 136     /label= E136D
FT      Misc-difference 153     /label= I153T
XX
PN      EP857788-A2.
PD      12-AUG-1998.
XX
PF      20-NOV-1997; 97EP-00309365.
XX
PR      21-NOV-1996; 96JP-00311103.
PR      18-JUN-1997; 97JP-00161674.
XX
PA      (AJIN ) AJINOMOTO CO INC.
XX
PI      Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
DR      WPI; 1998-416010/36.
XX
PT      Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
        with phosphate donor in presence of acid phosphatase - used as seasonings
        or pharmaceutical intermediates.

```

```

XX      XX      Example 19: Page: 83pp; English.
PS
CC      AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC      created using the mature protein of AAW71029. The specification describes
CC      a method for the preparation of nucleoside 5'-phosphate esters. The
CC      method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC      5.5 in the presence of an acid phosphatase that has been altered to
CC      increase its affinity for the nucleoside and/or to increase its thermal
CC      stability, or in the presence of a microorganism that has been
CC      transformed with recombinant DNA containing a gene coding for such an
CC      acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC      pharmaceuticals or as intermediates for them. note: this sequence does
CC      not appear in the specification; it was created using information
        provided
XX
SQ      Sequence 231 AA;
XX
Query Match      89.6%; Score 1051; DB 2; Length 231;
Best Local Similarity 89.0%; Pred. No. 2.6e-105;
Matches 203; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY      1 LVPAQNDATTYPDLYLLKNQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTTERGK 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3 LVATGNDTTTKPDLYLLKNSEAINSLALPPPPAVGSIAPFNDQAMYEQGRLLRNTTERGK 62
QY      61 LAEPDANLSAGVANAFFSAGFSPITTEKDAPOLHKLTLNMTEDAGDLATRSKEXMYRIR 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 QOQADADLAAGDVANAFFSAGFSPITTEKDAPOLHKLTLNMTEDAGDLATRSKEXMYRIR 122
QY      121 PFAFYGVSTCNTTTEODKLSKNGSYSPGHTSIGMATALVLAIEINPQRONEILKRGYELGES 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123 PFAFYGVSTCNTKDDKLSKNGSYSPGHTSIGMATALVLAIEINPQRONEILKRGYELGES 182
QY      181 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEPAKTOK 228
        |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      183 RVICGYHMOSDVAARIYGSAAVATLHTNPAFOOQLQKAKDEPAKTOK 230

```

Search completed: March 2, 2005, 20:22:55
Job time : 117.732 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:06 ; Search time 113.255 Seconds
(without alignments)

1030.896 Million cell updates/sec

Title: US-09-807-990A-125
Perfect score: 1173
Sequence: 1 LVPAQNDAITKPDLYLKNA.....NPAFOOOLQKAKDEFKATQK 228

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173	100.0	248	2	Q9FIU1 enterobacte
2	1136	96.8	248	2	Q9FIU0 klebsiella
3	1108	94.5	248	2	Q9RIW6 klebsiella
4	1091	93.0	249	2	Q9SIK6 escherichia
5	1046	89.2	249	2	Q9Q942 shigella fl
6	1043	88.9	249	2	Q9Q9Q9 shigella fl
7	1035	88.2	248	1	PHON PROST
8	983.5	83.8	249	1	PHOC MORMO
9	773	65.9	263	2	Q87188 prevotella
10	579.5	49.4	246	2	Q9Q9G5 shigella fl
11	574.5	49.0	246	2	Q9Q9G9 shigella fl
12	573.5	48.9	246	2	Q931G8 escherichia
13	568.5	48.5	246	2	Q6XW11 shigella fl
14	495.5	42.2	280	2	Q6AKP1 desulfofale
15	483	41.2	250	1	PHON SALTU
16	477.5	40.7	250	2	Q8KRT6 salmonella
17	476.5	40.6	250	2	PHON SALTU
18	476.5	40.6	250	2	Q7IEB8 salmonella
19	474	40.4	285	2	Q8PE10 xanthomonas
20	465.5	39.7	283	2	Q6AKN1 desulfofale
21	464.5	38.7	280	2	Q8P342 xanthomonas
22	417.5	35.6	289	2	Q7TU08 xanthomonas
23	341.5	29.1	264	1	PPA_ZYMO
24	274.5	23.4	258	2	Q9AB73 caulobacter
25	214	18.2	231	2	Q98HU7 rhizobium 1
26	189	16.1	423	2	Q814D5 salmonella
27	186	15.9	2314	2	Q69822 streptomyces
28	165	14.1	596	2	Q65GK3 bacillus li
29	161	13.7	241	2	Q916U4 pseudomonas
30	160	13.6	435	2	Q6DSH8 erwinia car
31	156	13.3	643	2	Q6FDK0 acinetobact

32	151	12.9	591	2	Q97124 clostridium
33	147.5	12.6	657	2	Q8Y350 ralsonia s
34	147	12.5	660	2	Q8U788 agrobacteri
35	146.5	12.5	128	2	Q7TUJ7 prochloroco
36	145.5	12.4	491	2	Q6A6B5 propionibac
37	138	11.8	986	2	Q87U02 pseudomonas
38	135	11.5	513	2	Q8G856 bifidobacte
39	134	11.4	115	2	Q6ZXV7 pseudomonas
40	134	11.4	115	2	Q6ZXW1 pseudomonas
41	133	11.3	115	2	Q6ZXW2 pseudomonas
42	133	11.3	622	2	Q8NR65 corynebacte
43	131	11.2	115	2	Q6ZXV6 pseudomonas
44	129	11.0	115	2	Q6ZXV8 pseudomonas
45	109.5	9.3	151	2	Q8KFG2 chlorobium

ALIGNMENTS

RESULT 1

Q9FIU1 PRELIMINARY; PRT; 248 AA.

AC Q9FIU1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Acid phosphatase.
GN Name-pho;
OS Enterobacter aerogenes (Enterobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
CX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12010;
RA Minara Y., Utagawa T., Matsui H., Amano Y.,
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044338; BAB18917.1; -.
DR HSSP; Q9SIA6; 1D2T.
DR GO; GO:00030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:00039933; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Ptase_C18A.
DR InterPro; IPR001011; Bac_AcPataase.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2_1.
DR PIRSF; PIRSF008977; Acid_Ptase_C18A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac_AcPataaseA; 1.
DR SMART; SM00014; acidPfc; 1.
DR PROSITE; PS01157; ACID_PHOSP_C1_A; 1.
SQ SEQUENCE 248 AA; 26563 MW; 20EFA2C285EE62D CRC64;

Query Match 100.0%; Score 1173; DB 2; Length 248;
Best Local Similarity 100.0%; Pred.No. 7.8e-97;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LVPAQNDAITKPDLYLKNAQIDSLALPPPEVGSIAFLNDQAMTEKGLLNTTERGK 60
DB	21	LVPAQNDAITKPDLYLKNAQIDSLALPPPEVGSIAFLNDQAMTEKGLLNTTERGK 80
QY	61	LAADANLISAGVANNASAFSGSPITEKDAPOQLKLTNNMEDGDLATRSKEXYRIR 120
DB	81	LAADANLISAGVANNASAFSGSPITEKDAPOQLKLTNNMEDGDLATRSKEXYRIR 140
QY	121	PPAFYGVSTCNTTEBQDKLSKNGSYPSGHTSIGATATVLAIEINPQRONEILKRGYELGES 180
DB	141	PPAFYGVSTCNTTEBQDKLSKNGSYPSGHTSIGATATVLAIEINPQRONEILKRGYELGES 200
QY	181	RVIIGYHMQSDVDAAKIVGSAVATLTNTNPAFOOOLQKAKDEFKATQK 228
DB	201	RVIIGYHMQSDVDAAKIVGSAVATLTNTNPAFOOOLQKAKDEFKATQK 248

```

RESULT 2
O991U0      PRELIMINARY;      PRT;      248 AA.
AC O991U0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Acid phosphatase.
GN Name-pho;
OS Klebsiella planticola (Raoultella planticola).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoultella.
OX NCBI_TaxID=575;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR HSSP; O9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008934; AcPase_VanPase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHRTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
SQ SEQUENCE 248 AA; 26745 MW; 68F65CA2448EB3EF CRC64;

Query Match
Best Local Similarity 96.8%; Score 1136; DB 2; Length 248;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LVPAQNDATTPDLYLTKNAQATDSLALPPPEVGSIAFLINDQMYEKGRLNTERGK 60
DB 21 LVPAQNDATTPDLYLTKNAQATDSLALPPPEVGSIAFLINDQMYEKGRLNTERGK 80
OY 61 LAADANLSAGVANAFSAFSGSPITEKAPOLHKLNTNIEDAGDLATRSAREKVRIR 120
DB 81 LAADANLSAGVANAFSAFSGSPITEKAPOLHKLNTNIEDAGDLATRSAREKVRIR 140
OY 121 PFAFYGVSTCNTTEEDKLSKNGSYSGHTSGMATLVLAELINPQRONEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEEDKLSKNGSYSGHTSGMATLVLAELINPQRONEILKRGYELGES 200
OY 181 RVICGYHMQSDVDPAARIVGSAVAVATLHTNPAFOOQLOKAKDEFKAKOK 228
DB 201 RVICGYHMQSDVDPAARIVGSAVAVATLHTNPAFOOQLOKAKDEFKAKOK 248

RESULT 3
O991U6      PRELIMINARY;      PRT;      248 AA.
AC O991U6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Phoc protein precursor (EC 3.1.3.2).
GN Name-phoc;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG 225;
RA Passariello C., Berlutti F., Selan L., Thaller M.C., Rossolini G.;

```

```

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250377; CAB59725.1; -.
DR HSSP; O9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008934; AcPase_VanPase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHRTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
FT SIGNAL 1
FT CHAIN 21
SQ SEQUENCE 248 AA; 27110 MW; ED6E9D8663636BDD CRC64;

Query Match
Best Local Similarity 94.5%; Score 1108; DB 2; Length 248;
Matches 215; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 LVPAQNDATTPDLYLTKNAQATDSLALPPPEVGSIAFLINDQMYEKGRLNTERGK 60
DB 21 LVPAQNDATTPDLYLTKNAQATDSLALPPPEVGSIAFLINDQMYEKGRLNTERGK 80
OY 61 LAADANLSAGVANAFSAFSGSPITEKAPOLHKLNTNIEDAGDLATRSAREKVRIR 120
DB 81 LAADANLSAGVANAFSAFSGSPITEKAPOLHKLNTNIEDAGDLATRSAREKVRIR 140
OY 121 PFAFYGVSTCNTTEEDKLSKNGSYSGHTSGMATLVLAELINPQRONEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEEDKLSKNGSYSGHTSGMATLVLAELINPQRONEILKRGYELGES 200
OY 181 RVICGYHMQSDVDPAARIVGSAVAVATLHTNPAFOOQLOKAKDEFKAKOK 228
DB 201 RVICGYHMQSDVDPAARIVGSAVAVATLHTNPAFOOQLOKAKDEFKAKOK 248

RESULT 4
O9S1A6      PRELIMINARY;      PRT;      249 AA.
AC O9S1A6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Acid phosphatase (EC 3.1.3.2).
GN Name-pho;
OS Escherichia blattae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=563;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM1650;
RA MEDLINE=20296667; PubMed=10835340; DOI=10.1093/emboj/19.11.2412;
RA Ishikawa K., Mihara Y., Gondoh K., Suzuki E., Asano Y.;
RT "X-ray structures of a novel acid phosphatase from Escherichia blattae
and its complex with the transition-state analog molybdate."
RL EMBO J. 19:2412-2423 (2000).
DR EMBL; AB020481; BAA84942.1; -.
DR PDB; 1D2T; X-ray; A=19-249.
DR PDB; 1E01; X-ray; A/B/C=19-249.
DR PDB; 1IW8; X-ray; A/D/E=19-249, B/C/F=-.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR InterPro; IPR01158; Acid_Phase_C1A.
DR InterPro; IPR008934; AcPase_VanPase.
DR InterPro; IPR001011; Bac_AcPaseA.

```


DR InterPro; IPR000326; Peesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C18A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac_AcPataase; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSP CL_A; 1.
DR Hydrolase.
SQ SEQUENCE 249 AA; 26956 MW; 7ABAE6CB61FC0CA3 CRC64;

Query Match 93.0%; Score 1091; DB 2; Length 249;
Best Local Similarity 92.1%; Pred. No. 1.8e-89;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
DB 21 LVATGNDTTPDLYLLKNSKSHNSLALPPPAVGSIAFLNDQAMYEKGRLLRTERGK 80
QY 61 LAEDANLSAGVANAFSSAFSPITTEKDAPOHLKLTNMTEDAGDLATRSKKEKYMIR 120
DB 81 LAEDANLSAGVANAFSSAFSPITTEKDAPOHLKLTNMTEDAGDLATRSKKEKYMIR 140
QY 121 PFAFGVSTCNTTKEDDKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 180
DB 141 PFAFGVSTCNTTKEDDKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 200
QY 181 RVICGYHQSDVDARIVGSAVAVATLHTNPAFOOOLQKAKDEFATOK 228
DB 201 RVICGYHQSDVDARIVGSAVAVATLHTNPAFOOOLQKAKDEFATOK 248

RESULT 5

ID 050542 PRELIMINARY; PRT; 249 AA.

AC 050542;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Nonspecific phosphatase.
GN Name=phon;
OS Shigella flexneri.
OC Plasmid pMYSH6000.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxId=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YSH6000;
RX MEDLINE=96345620; PubMed=8755883;
RA Uchiya K., Tohnoji M., Nikai T., Sugihara H., Sasakawa C.;
RT "Identification and characterization of phon-sf, a gene on the large
plasmid of Shigella flexneri 2a encoding a nonspecific phosphatase.";
RL J. Bacteriol. 178:4548-4554(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=YSH6000;
RA Uchiya K.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D82966; BA011655.1; -.
DR HSSP; Q9S1A6; 1D2T.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Phase_C18A.
DR InterPro; IPR00834; AcPase_VanPase.
DR InterPro; IPR001011; Bac_AcPataase.
DR InterPro; IPR000326; Peesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C18A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac_AcPataase; 1.
DR SMART; SM00014; acidPpc; 1.
DR PROSITE; PS01157; ACID_PHOSP CL_A; 1.
KM Plasmid.

SQ SEQUENCE 249 AA; 27177 MW; 58F34CEB034EB070 CRC64;

Query Match. 89.2%; Score 1046; DB 2; Length 249;
Best Local Similarity 87.2%; Pred. No. 1.9e-85;
Matches 198; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 2 VPAGNDATTKPDLYLLKNAQAIDSLALLPPPEVGSIAFLNDQAMYEKGRLLRTERGK 61
DB 22 IPGNDVTTKPDLYLLTNDNAIDSLALLPPPGIGSIAFLNDQAMYEKGRLLRTERGK 81
QY 62 AEDANLSAGVANAFSSAFSPITTEKDAPOHLKLTNMTEDAGDLATRSKKEKYMIR 121
DB 82 AEDANLSAGVANAFSSAFSPITTEKDAPOHLKLTNMTEDAGDLATRSKKEKYMIR 141
QY 122 PAFGVSTCNTTKEDDKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 181
DB 142 PAFGVSTCNTTKEDDKLSKNGSYSGHTSIGMATLVLAELNPOREILKRGYELGSR 201
QY 182 VICGYHQSDVDARIVGSAVAVATLHTNPAFOOOLQKAKDEFATOK 228
DB 202 VICGYHQSDVDARIVGSAVAVATLHTNPAFOOOLQKAKDEFATOK 248

RESULT 6

ID 099099 PRELIMINARY; PRT; 249 AA.

AC 099099; 07BCK1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Phon1, periplasmic non specific acid ohosphatase (Phosphatase
precursor).
GN Name=phon1; Synonyms=phon-sf;
OS Shigella flexneri.
OC Plasmid virulence plasmid pWR501, and plasmid pCP301.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxId=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T;
RX MEDLINE=20566792; PubMed=1115111;
RA Buchrieser C., Glaeser P., Rusnick C., Nedjari H., d'Hauteville H.,
RA Kunst F., Sansonetti P., Parosot C.;
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
by the type III secretion apparatus of Shigella flexneri.";
RL Mol. Microbiol. 38:760-771(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=virulence plasmid pWR501;
RX MEDLINE=2189246; PubMed=11297750;
RX DOI=10.1128/JAI.69.5.3271-3285.2001;
RA Verkaesbean M.M., Goldberg M.B., Rose D.J., Grotbeck B.J., Burland V.,
RA Blatner F.R.;
RT "Complete DNA sequence and analysis of the large virulence plasmid of
Shigella flexneri.";
RL Infect. Immun. 69:3271-3285(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a; PLASMID=pCP301;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
DR EMBL; AL391753; CAC05839.1; -.
DR EMBL; AF348706; AK18512.1; -.
DR EMBL; AF386526; AAL72311.1; -.
DR HSSP; Q9S1A6; 1D2T.

DR GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro: IPR011158; Acid_Ptase_C1aB.
 DR InterPro: IPR008934; AcPase_VanPterase.
 DR InterPro: IPR010111; Bac_AcPataaseA.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Ptase_C1aA_1.
 DR PRINTS: PR00483; BACPHPTASE.
 DR Prodom: PD009838; Bac_AcPataaseA.
 DR SMART: SM00014; acidPfc_1.
 DR SWART: SM00014; acidPfc_1.
 DR PROSITE: PS01157; ACID_PHOSPH_CL_A_1.
 DR Complete proteome; Plasmid.
 SQ SEQUENCE 249 AA; 27211 MW; 9051C6C1CE21ABA CRC64;

Query Match 88.9%; Score 1043; DB 2; Length 249;
 Best Local Similarity 87.6%; Pred. No. 3.5e-85;
 Matches 188; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 3 PACNDATTKRDLVYLKNAQIDSLALLPPEVEGSIATFNDQMYEKRLRTERGKLA 62
 DB 23 PPGNDVTTKRDLYLTLNDAIDSLALLPPEPGISATFNDQMYEKRLRTERGKLA 82
 QY 63 AEDANISAGGVANAFSSAFSGPTTEKDAFQHLKLTNMTEDAGDLATRSKAKYMRIRP 122
 DB 83 AEDANISAGGVANAFSSAFSGPTTEKDAFQHLKLTNMTEDAGDLATRSKAKYMRIRP 142
 QY 123 AFYGVSTCNTBEDKLSKNGSYPSGHTSIGMATVLAELINPQRONEILKRGYELGESR 182
 DB 143 AFYGVSTCNTBEDKLSKNGSYPSGHTSIGMATVLAELINPQRONEILKRGYELGESR 202
 QY 183 ICGYHMQSDVDARIVGSAVATLTNPAFQOOLQAKDEFAKTOK 228
 DB 203 ICGYHMQSDVDARIVGSAVATLTNPAFQOOLQAKDEFAKTOK 248

RESULT 7
 PHOC_PROST STANDARD; PRT; 248 AA.
 ID PHOC_PROST
 AC P26975;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
 GN Name=phoc;
 OS Providencia stuartii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Providencia.
 OX NCBI_TaxID=588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PV81;
 RA Riccio M.L., Lombardi G., Chiesurin A., Satta G.;
 RL Submitted (FEB-1992) to the EMBL/Genbank/DBP databases.
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).

EMBL: X64820; CAA46032.1; -
 PIR: S19888; PROCS.
 HSP: O951A6; 1D2T.
 DR InterPro: IPR011158; Acid_Ptase_C1aA.
 DR InterPro: IPR008934; AcPase_VanPterase.

DR InterPro: IPR001011; Bac_AcPataaseA.
 DR InterPro: IPR000326; Pesterase_PA_PTP.
 DR Pfam: PF01569; PAP2_1.
 DR PIRSF: PIRSF000897; Acid_Ptase_C1aA_1.
 DR PRINTS: PR00483; BACPHPTASE.
 DR Prodom: PD009838; Bac_AcPataaseA.
 DR SMART: SM00014; acidPfc_1.
 DR PROSITE: PS01157; ACID_PHOSPH_CL_A_1.
 DR Hydrolyase; Periplasmic; Signal.
 FT SIGNAL 1
 FT CHAIN 21
 SQ SEQUENCE 248 AA; 27043 MW; 2122A4B95E767CB2 CRC64;

Query Match 88.2%; Score 1035; DB 1; Length 248;
 Best Local Similarity 85.5%; Pred. No. 1.8e-84;
 Matches 194; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 2 VPAGNDATTKRDLVYLKNAQIDSLALLPPEVEGSIATFNDQMYEKRLRTERGKLA 61
 DB 22 IPPGNDVTTKRDLYLTLNDAIDSLALLPPEVEGSIATFNDQMYEKRLRTERGKLA 81
 QY 62 AEDANISAGGVANAFSSAFSGPTTEKDAFQHLKLTNMTEDAGDLATRSKAKYMRIRP 121
 DB 82 AAKDADLAAGGVANAFSSAFSGPTTEKDAFQHLKLTNMTEDAGDLATRSKAKYMRIRP 141
 QY 122 AFYGVSTCNTBEDKLSKNGSYPSGHTSIGMATVLAELINPQRONEILKRGYELGESR 181
 DB 142 AFYGVSTCNTBEDKLSKNGSYPSGHTSIGMATVLAELINPQRONEILKRGYELGESR 201
 QY 182 VICGYHMQSDVDARIVGSAVATLTNPAFQOOLQAKDEFAKTOK 228
 DB 202 VICGYHMQSDVDARIVGSAVATLTNPAFQOOLQAKDEFAKTOK 248

RESULT 8
 PHOC_MORMO STANDARD; PRT; 249 AA.
 ID PHOC_MORMO
 AC P28581;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Major phosphate-irrepressible acid phosphatase precursor (EC 3.1.3.2) (HPAP).
 GN Name=phoc;
 OS Morganella morganii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.
 RC STRAIN=RS12;
 RA MEDLINE=94362901; PubMed=8081499;
 RA Thaller M.C., Berlucchi F., Schippa S., Lombardi G., Rossolini G.M.;
 RT "Characterization and sequence of phoc, the principal phosphate-
 RT irrepressible acid phosphatase of Morganella morganii.",
 RL Microbiology 140:1341-1350 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 10466;
 RX MEDLINE=20336426; PubMed=10877772;
 RX DOI=10.1128/AEM.66.7.2811-2816.2000;
 RA Mhara Y., Utagawa T., Yamada H., Asano Y.;
 RT "Phosphorylation of nucleosides by the mutated acid phosphatase from
 RT Morganella morganii.",
 RL Appl. Environ. Microbiol. 66:2811-2816 (2000).
 CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
 CC phosphate.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- MISCELLANEOUS: Has a pH optimum around 6.
 CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase
 CC family.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64444; CA45774.1; -
DR EMBL; AB035805; BA96744.1; -
DR PIR; S19187; S19187.
DR HSSP; Q9S1A6; 1D2T.
DR InterPro; IPR011158; Acid_Please_C1A.
DR InterPro; IPR008934; AcPase_VanPase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Please_C1A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPfc; 1.
DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
DR Direct protein sequencing; Hydrolyase; Periplasmic; Signal.
KW SIGNAL
FT CHAIN 1 20
FT SIGNAL 21 249
SQ SEQUENCE 249 AA; 26998 MW; C43P368052B6A5C CRC64;
Major phosphate-irrepressible acid
phosphatase.
Query Match 83.8%; Score 983.5; DB 1; Length 249;
Best Local Similarity 82.9%; Pred. No. 7.6e-80;
Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;
QY 2 VPAGNDATTKEDLYLTKNAQADSLALPPPEVGSIAFLNDQAMYEKGRLLNTERGKLAEDA 61
DB 22 IPAGNDATTKEDLYLTKNEQALDSLALPPPEVGSIOFLNDQAMYEKGRLLNTERGKQ 81
QY 62 AADANLISAGVANAFASSAFSPITEKDAPOHLKLTNNIEDAGDLATRSAXEKYRIRP 121
DB 82 AQADADDLAAGVATNFSGAFGPIREKOSPFLYKLTNNIEDAGDLATRSAXEHMRIRP 141
QY 122 FAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETINPORONEILKRGVELGSSR 181
DB 142 FAFYGVSTCNTTKDQKLSKNGSPSGHTSIGMATLVLAETINPORONEILKRGVELGSSR 201
QY 182 VICGHWQSDVDARIVGSAVAVATHTNPAFOOQLKAKDEFKAKTOK 228
DB 202 VICGHWQSDVDARIVGSAVAVATHTNPAFOOQLKAKDEFKAKTOK 249
RESULT 9
087188 PRELIMINARY; PRT; 263 AA.
AC 087188;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Acid phosphatase (PACP) precursor.
GN Name=PnOC;
OS Prevotella intermedia.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Prevotellaceae; Prevotella.
OX NCBI_TaxID=28131;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25611;
RX MEDLINE=20026825; PubMed=10559178;
RA Chen X., Ansat T., Awano S., Iida T., Barik S., Takehana T.;
RT "Isolation, cloning, and expression of an acid phosphatase containing
RT phosphotyrosyl phosphatase activity from Prevotella intermedia.";
RL J. Bacteriol. 181:7107-7114 (1999).
DR EMBL; AB017537; BA43148.1; -
DR HSSP; Q9S1A6; 1D2T.
GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.

DR GO; GO:0030288; F:acid phosphatase activity; IEA.
DR InterPro; IPR011158; Acid_Please_C1A.
DR InterPro; IPR008934; AcPase_VanPase.
DR InterPro; IPR001011; Bac_AcPaseA.
DR InterPro; IPR000326; Pesterase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Please_C1A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009838; Bac_AcPaseA; 1.
DR SMART; SM00014; acidPfc; 1.
DR PROSITE; PS01157; ACID_PHOSP_CL_A; 1.
KW Signal.
FT SIGNAL 1 20
SQ SEQUENCE 263 AA; 29201 MW; 6AD1C4A6470BF313 CRC64;
Potential.
Query Match 65.9%; Score 773; DB 2; Length 263;
Best Local Similarity 65.8%; Pred. No. 6.1e-61;
Matches 146; Conservative 29; Mismatches 47; Indels 0; Gaps 0;
QY 7 DATKPDLYLTKNAQADSLALPPPEVGSIAFLNDQAMYEKGRLLNTERGKLAEDA 66
DB 29 DARNPDLYLTKDQQTSSLELPPPEVGSIOFLYDEAOYQKGMQNTREGDQAVADA 88
QY 67 NLSAGVANAFASSAFSPITEKDAPOHLKLTNNIEDAGDLATRSAXEKYRIRPFAFG 126
DB 89 RVGGDGVNNAFSAFAGIKSKETTPFIKLVNREDAQDLATRSAXKHVVRVFPFAYN 148
QY 127 VSTCNTTEODKLSKNGSPSGHTSIGMATLVLAETINPORONEILKRGVELGSSR 186
DB 149 EMTCNPEQOQLSTNGSPSGHTSIGMATLVLAETINPORONEILKRGVELGSSR 208
QY 187 HMOSDVDAARIVGSAVAVATHTNPAFOOQLKAKDEFKAKTOK 228
DB 209 HMOSDVDAARIVGSAVAVATHTNPAFOOQLKAKDEFKAKTOK 250
RESULT 10
0990G5 PRELIMINARY; PRT; 246 AA.
AC 0990G5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Phn2 (Apy), periplasmic phosphatase, apyrase, ATP diphosphohydrolase
(Apyrase).
GN Name=phn2 (apy); Synonym=S0004;
OS Shigella flexneri.
OC Plasmid virulence plasmid pMR501.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T;
RX MEDLINE=20566792; PubMed=1115111;
RA Buchrieser C., Glaeser P., Rusnik C., Nedjari H., d'Hauteville H.,
RA Kunst F., Sansonetti P., Parosot C.;
RT "The virulence plasmid pMR100 and the repertoire of proteins secreted
RT by the type III secretion apparatus of Shigella flexneri.";
RL Mol. Microbiol. 38:760-771 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=virulence plasmid pMR501;
RX MEDLINE=21189246; PubMed=11292750;
RX DOI=10.1128/JAI.69.5.3271-3285.2001;
RA Verkacean M.M., Goldberg M.B., Rose D.J., Groetbeck E.J., Burland V.,
RA Blatter F.R.;
RT "Complete DNA sequence and analysis of the large virulence plasmid of
RT Shigella flexneri.";
RL Infect. Immun. 69:3271-3285 (2001).
DR EMBL; AL391753; CAC05771.1; -
DR EMBL; AF348706; AAK18315.1; -
DR HSSP; Q9S1A6; 1IWS.

DR GO:0003288; C-periplasmic space (sensu Gram-negative Bact. ., IEA.
DR GO:0003992; F-acid phosphatase activity, IEA.
DR GO:0016787; Phosphatase activity, IEA.
DR InterPro: IPR01158; Acid_Phase_Class.
DR InterPro: IPR008934; AcPase_VanBerase.
DR InterPro: IPR001011; Bac_AcPasease.
DR InterPro: IPR000326; Pesterase_PA_PTP.
DR Pfam: PF01569; PAR2; 1.
DR PIRSF: PIRSF000897; Acid_Phase_Class; 1.
DR PRINTS: PR00483; BACPHASE.
DR ProDom: PD009838; Bac_AcPasease; 1.
DR SMART: SM00014; acidPpc; 1.
DR HydroLase; Plasmid.
SQ SEQUENCE 246 AA; 27559 MW; 48D76BD8CC7885E5 CRC64;

Query Match: 49.4%; Score 579.5; DB 2; Length 246;
Best Local Similarity 50.9%; Pred. No. 1.2e-43;
Matches 113; Conservative 40; Mismatches 64; Indels 5; Gaps 2

QY 2 VPAGNDATTKPDLVYLKNAQATIDSLALPPPEVGSIFLINDQAMYEGRLIRNTERKTL 61
DB 18 IPSANALAKAE---FLTQGTSPDLSILPPPAEDSVYFLADKAHYEGRSLRDNRRVL 74
QY 62 AAEDNALSAGVANAFFSSAFSGPITEKAPQLHKLITNMIEDAGDLATRSAREKRYTRP 121
DB 75 ASEBAAYENFGI--AFSDAYGMDISRENTPIYLQTLTVLQSHDYAVRNAKEYKRVRP 132
QY 122 FAFYGVSTCNTTEODKLSKNSYSPGHSIGMATVLYAENPQONITLRGYLGEGR 181
DB 133 FVIYKDAICTCTDCKEKKAITGTSYSGHASFGAAVALLIATINPORKAIELIRGYEFGESR 192
QY 182 VICGHWQSDVDAAARIVSAAVATLHTNPAFOQLQAKDEP 223
DB 193 VICGAHWQSDVEAGRLMGASVAVLHNPETFTKLSSEAKKEF 234

RESULT 11
Q59909 PRELIMINARY; PRT; 246 AA.
AC Q59909; Q7BCQ3;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 25-OCT-2004 (TREMBLrel. 26, Last annotation update)
DE AP di-phosphohydrolase, apyrase precursor (EC 3.6.1.5) (Apyrase).
GN Name=apyr;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_Taxid=623;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=2a;
RA Ramchandran V., Sankaran K., Subrahmanyam Y.V.B.K., Ramakrishnan R.,
RA Datta S., Roy R.K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=2a;
RA Roy R.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / serotype 2a; PLASMID=pcp301;
RC MEDLINE=22272406; PubMed=12384550; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Sun L., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RT Nucleic Acids Res. 30:4432-4441(2002).

EMBL; U04539; AAA1206.1; -.
DR EMBL; AF386526; AAL72358.1; -.
DR HSSP; Q9S1A6; 11W6.
DR GO; GO:0030284; C:periplasmic space (sensu Gram-negative Bact. . ; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0004050; P:phosphatase activity; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPRO11158; Acid_Phase_C1A.
DR InterPro; IPRO08934; AcPase_VanPase.
DR InterPro; IPRO01011; Bac_AcPase.
DR InterPro; IPRO00326; Peptidase_PA_PTP.
DR Pfam; PF01569; PAP2; 1.
DR PIRSF; PIRSF000897; Acid_Phase_C1A; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac_AcPaseA; 1.
DR SMART; SMO0014; acidPhC_1.
KM Complete proteome; Hydrolase; Signal.
FT SIGNAL 1 Potential.
SQ SEQUENCE 246 AA; 237573 MW; B81737D9E6143912 CRC64;

Query Match 49.0%; Score 574.5; DB 2; Length 246;
Best Local Similarity 50.5%; Pred. No. 3.5e-43;
Matches 112; Conservative 40; Mismatches 65; Indels 5; Gaps 2;

DY 2 VPAGNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGKL 61
DB 18 IPSANALKAE--FLTQTSPDSLSILPPPAENSVVFQADKAHYEGSRGLRANVRLL 74
DY 62 AAEQNLSAGGVANAFAFSAPSPTEKDAPOLHLLTNMEDAGDLATRASKETMRIRP 121
DB 75 ASEDIYYENFGL-AFSDAYCMDISRENTPLTYOLLTQVODSHDYAVRNAKETKKVRP 132
DY 122 FAFYGVSTCNTEDPKLSKNKSYSGHTSGMATLVLAIEINPORONEILIKRGVELGSR 181
DB 133 FVIYKDATCTCPDDKEKVALIGSYSGASHSCGMANALLIABINPRKAEILLRGTFESRR 192
DY 182 VICGYHWOSVDPARIVGSAVVATLTHTNPAPFOQLQKAKEF 223
DB 193 VTCGAHWOSDVDEAGRLMGASVVAVLNHTPEFTSLSEAKKEF 234

RESULT 12
Q9J1G8 PRELIMINARY; PRT; 246 AA.

ID Q9J1G8
AC Q9J1G8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AprYase (EC 3.6.1.5).
GN Name=apy;
OS Escherichia coli.
OC Plasmid PHN280.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HN280;
RX MEDLINE=22167055; PubMed=12177345;
RA Santapaula D., Casallino M., Petrucca A., Presutti C., Zagaglia C.,
Berluti F., Colonna B., Nicoletti M.;
RT "Enteroinvasive Escherichia coli virulence-plasmid-carried apyrase
(apy) and ospB genes are organized as a bicistronic operon and are
subject to differential expression.";
RT Microbiology 148:2519-2529(2002).
RL EMBL; AJ315184; CAC67470.1; -.
DR EMBL; Q9S1A6; 11W6.
DR HSSP; Q9S1A6; 11W6.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . ; IEA.
DR GO; GO:0003993; F:acyclate phosphatase activity; IEA.
DR GO; GO:0004050; P:acyclate activity; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPRO11158; Acid_Phase_C1A.
DR InterPro; IPRO08934; AcPase_VanPase.
DR InterPro; IPRO00934; AcPase_VanPase.

DR InterPro; IPR001011; Bac AcPcaseA.
 DR InterPro; IPR000326; Peesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid_Please_CLA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac AcPcaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 KM HydroLase; Plasmid.
 SQ SEQUENCE 246 AA; 27574 MW; DAIF901BEB075F4 CRC64;

Query Match 48.9%; Score 573.5; DB 2; Length 246;
 Best Local Similarity 50.5%; Pred. No. 4,3e-43;
 Matches 112; Conservative 40; Mismatches 65; Indels 5; Gaps 2;

QY 2 VPAGNDATTKPDLYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERRKL 61
 DB 18 IPSANALKAEG---FLTQOTSPDISLILPPPAEDSVVFOADKAYEFGRLRDANRVRL 74
 QY 62 AAEDANLSAGVANAFSSAFSGPIITEKDAPOLHKLITNMIEDAGDLATRSAREKYMRIIP 121
 DB 75 ASEDAYENFGL--AFSDAYGMDISRENTPILYQLLTVDLSDHYAVRNAREYKRYRP 132
 QY 122 PAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGSR 181
 DB 133 FVIYKDATCTPDKDEKMAITGSPSGHASFQWAVALLAEINPQKAEILRGRYEFGEGR 192
 QY 182 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEF 223
 DB 193 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEF 224

RESULT 13

ID 06XW11 PRELIMINARY; PRT; 246 AA.
 AC 06XW11;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Phn2.
 GN Name=Phn2;
 OS Shigella flexneri.
 OC Plasmid pINV P6 M1382.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935215; PubMed=14573649;
 RX DOI=10.1128/IAI.71.11.6298-6306.2003;
 RA Lan R., Stevenson G., Reeves P.R.,
 RT "Comparison of two major forms of the Shigella virulence plasmid pINV:
 RT positive selection is a major force driving the divergence".
 RL Infect. Immun. 71:6298-6306(2003).
 DR EMBL; AY206428; AAP78968.1; .
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR01158; Acid_Please_CLA.
 DR InterPro; IPR00834; AcPase VanPase.
 DR InterPro; IPR001011; Bac AcPcaseA.
 DR InterPro; IPR000326; Peesterase_PA_PTP.
 DR PIRSF; PIRSF000897; Acid_Please_CLA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac AcPcaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 KM Plasmid.
 SQ SEQUENCE 246 AA; 27560 MW; DASE971B99B70583 CRC64;

Query Match 48.5%; Score 568.5; DB 2; Length 246;
 Best Local Similarity 50.0%; Pred. No. 1.2e-42;
 Matches 111; Conservative 40; Mismatches 66; Indels 5; Gaps 2;
 QY 2 VPAGNDATTKPDLYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERRKL 61
 DB 18 IPSANALKAEG---FLTQOTSPDISLILPPPAEDSVVFOADKAYEFGRLRDANRVRL 74

DB 18 IPSANALKAEG---FLTQOTSPDISLILPPPAEDSVVFOADKAYEFGRLRDANRVRL 74
 QY 62 AAEDANLSAGVANAFSSAFSGPIITEKDAPOLHKLITNMIEDAGDLATRSAREKYMRIIP 121
 DB 75 ASEDAYENFGL--AFSDAYGMDISRENTPILYQLLTVDLSDHYAVRNAREYKRYRP 132
 QY 122 PAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGSR 181
 DB 133 FVIYKDATCTPDKDEKMAITGSPSGHASFQWAVALLAEINPQKAEILRGRYEFGEGR 192
 QY 182 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEF 223
 DB 193 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEF 224

RESULT 14

ID 06AKP1 PRELIMINARY; PRT; 280 AA.
 AC 06AKP1;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Probable acid phosphatase.
 GN OrderedLocusNames=DP2355;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LSV54 / DSM 12343;
 RX PubMed=15305914;
 RA Rabus R., Ruepp A., Frickey T., Rätei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments".
 RL Environ. Microbiol. 6:887-902(2004).
 DR EMBL; CR522870; CAG37084.1; .
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR01158; Acid_Please_CLA.
 DR InterPro; IPR00834; AcPase VanPase.
 DR InterPro; IPR001011; Bac AcPcaseA.
 DR InterPro; IPR000326; Peesterase_PA_PTP.
 DR Pfam; PF01569; PAP2; 1.
 DR PIRSF; PIRSF000897; Acid_Please_CLA; 1.
 DR PRINTS; PR00483; BACPHPTASE.
 DR ProDom; PD009838; Bac AcPcaseA; 1.
 DR SMART; SM00014; acidPfc; 1.
 DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
 KM Complete proteome.
 SQ SEQUENCE 280 AA; 30742 MW; C8231006557991F4 CRC64;

Query Match 42.2%; Score 495.5; DB 2; Length 280;
 Best Local Similarity 46.6%; Pred. No. 5e-36;
 Matches 103; Conservative 36; Mismatches 77; Indels 5; Gaps 2;

QY 6 NDATTKPDLYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERRKL 61
 DB 26 NDLPQIKVLVDGLVLDGLATDTPDLSALLPQPAKESTPFAIDREVSXKSLRLDTPARTL 85
 QY 62 AAEDANLSAGVANAFSSAFSGPIITEKDAPOLHKLITNMIEDAGDLATRSAREKYMRIIP 121
 DB 86 AARDARLTFPPQAAAFSCALGVPISEETPHLYMLRHTLTDA-LSTDKAKDNYRRTRP 144
 QY 122 PAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGSR 181
 DB 145 FVNGEPCVCTPDQSEOLKSGSPSGHTSIGMATLVLAELINPORONEILKRGYELGSR 204
 QY 182 VICGHWQSDVDAAIRIVGSAVVATLHTNPAFOOOLQAKDEF 222

DB 205 IVCNHWQSDVWGRIMGAIVARLHADPAFLAEIEVAKAE 245

RESULT 15

ID PHON_SALTY STANDARD: PRT; 250 AA.

AC P26976;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).

GN Name=phon; OrderedLocustNames=5TM4319;

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 14028 / SGSG 2980;

RX MEDLINE=92224869; PubMed=1339343;

RA Grolsman E.A., Saier M.H. Jr., Ochman H.;

RT "Horizontal transfer of a phosphatase gene as evidence for mosaic structure of the Salmonella genome.";

RL EMBO J. 11:1309-1316(1992).

RM [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2;

RX MEDLINE=92041557; PubMed=1938882;

RA Kaasahara M., Nakata A., Shinagawa H.;

RT "Molecular analysis of the Salmonella typhimurium phon gene, which encodes nonspecific acid phosphatase.";

RL J. Bacteriol. 173:6760-6765(1991).

RM [3]

RP SEQUENCE FROM N.A.

RC STRAIN=LT7 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";

RL Nature 413:852-856(2001).

CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol + phosphate.

CC -1- SUBUNIT: Homodimer (Probable).

CC -1- SUBCELLULAR LOCATION: Periplasmic.

CC -1- SIMILARITY: Belongs to the class A bacterial acid phosphatase family.

CC -1- CAUTION: Ref.2 sequence differs from that shown in the C-terminus due to a frameshift.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X63599; CAA45144.1; -;

DR EMBL; X59036; CAA41760.1; ALT_FRAME.

DR EMBL; AB008902; AAL23143.1; -;

DR PIR; S20958; A41330.

DR HSP; Q9S1A6; 11W8.

DR StyGene; SG10292; phon.

DR InterPro; IPR01158; Acid_Ptase_C1A.

DR InterPro; IPR008934; AcPase_Vanperase.

DR InterPro; IPR001011; Bac_AcPataaseh.

DR InterPro; IPR000326; Pesterase_PA_PTP.

DR Pfam; PF01569; PAP2; 1.

DR PIRSF; PIRSF00897; Acid_Ptase_C1A; 1.

DR PRINTS; PR00483; BACPHPTASE.

DR ProDom; PD009838; Bac AcPataase; 1.

DR SMART; SM00014; acidPc; 1.

DR PROSITE; PS01157; ACID_PHOSP_C1A; 1.

DR Complete proteome; Hydrolase; Periplasmic; Signal.

FT SIGNAL 1 20 potential.

FT CHAIN 21 250 Nonspecific acid phosphatase.

SQ SEQUENCE 250 AA; 28382 MW; CPE8DA409BD57573 CRC64;

Query Match 41.2%; Score 483; DB 1; Length 250;

Best Local Similarity 47.0%; Pred. No. 5.7e-35;

Matches 95; Conservative 33; Mismatches 74; Indels 0; Gaps 0;

QY 21 QAIISLALLPPPEVGSIAFLNDQMYEKRLNTERGKLAEDANLSAGVANNAPSSA 80

DB 31 ESNVSGPYLPPPPENDDPATRYDKEAYFKGYAIGSRKQAAEDADVSENIARISPV 90

QY 81 FGSPTKEKAPQLHKLITNMIEDAGDLATRSAREKYNRIRPFAYGVSTCNTTEQDKLSK 140

DB 91 VGAKINPKDPEETWNMLKNLLTWGGYATASAKKYVTRTPFVLFNHSCTRPEDENTLRK 150

QY 141 NGSPSGHTSGMTAVLAELNQRONEILKRGVEGESRVTCGYTQSDVDAARIYGS 200

DB 151 NGSYPSGHTYGTLLALVLSEARPERAQLARRGMEGQSRVTCGAHWQSDVDAGRYVGA 210

QY 201 AVVATLHTNPAPFOOQLOKADDE 222

DB 211 VEPARLOTIRAFQSLAKVREE 232

Search completed: March 2, 2005, 20:26:49

Job time : 114.255 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:26:57 ; Search time 86.4314 Seconds
(without alignments)
865.359 Million cell updates/sec

Title: US-09-807-990A-125

Perfect score: 1173

Sequence: 1 LVPAQNDATKPDLYYLKNA.....NDPAFQQLQKAKDEFAKTQK 228

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues
Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173	100.0	248	9	US-09-727-578-24 Sequence 24, Appl
2	1136	96.8	248	9	US-09-727-578-26 Sequence 26, Appl
3	1091	93.0	231	9	US-09-727-578-8 Sequence 8, Appl
4	1091	93.0	249	9	US-09-727-578-7 Sequence 7, Appl
5	1035	88.2	248	9	US-09-727-578-22 Sequence 22, Appl
6	983.5	83.8	229	9	US-09-727-578-4 Sequence 4, Appl
7	983.5	83.8	249	9	US-09-727-578-3 Sequence 3, Appl
8	983.5	83.8	249	16	US-10-220-481-116 Sequence 116, App
9	772	65.8	244	9	US-09-727-578-28 Sequence 28, Appl
10	133	11.3	622	9	US-09-738-626-4817 Sequence 4817, Ap
11	105	9.0	414	16	US-10-437-963-165801 Sequence 165801,
12	97	8.3	20	9	US-09-727-578-1 Sequence 1, Appl
13	96.5	8.2	647	16	US-10-437-963-112291 Sequence 112291,

14	96	8.2	178	15	US-10-282-122A-77490 Sequence 77490, A
15	93.5	8.0	528	15	US-10-424-599-210277 Sequence 210277,
16	93.5	8.0	611	15	US-10-424-599-210275 Sequence 210275,
17	93.5	8.0	611	15	US-10-425-114-49161 Sequence 49161, A
18	92	7.8	159	9	US-09-738-626-6679 Sequence 6679, Ap
19	92	7.8	159	15	US-10-627-476-102 Sequence 102, App
20	92	7.8	408	15	US-10-369-493-9754 Sequence 9754, Ap
21	90.5	7.7	921	14	US-10-281-866-2 Sequence 2, Appl
22	90	7.7	201	14	US-10-156-761-7677 Sequence 7677, Ap
23	90	7.7	437	15	US-10-282-122A-66585 Sequence 66585, A
24	90	7.7	1610	15	US-10-369-493-3448 Sequence 3448, Ap
25	89	7.6	608	9	US-10-369-493-5228 Sequence 5228, Ap
26	88.5	7.5	168	9	US-09-738-626-6676 Sequence 6676, Ap
27	88.5	7.5	1707	14	US-10-223-070-13 Sequence 13, Appl
28	88	7.5	265	15	US-10-434-599-243256 Sequence 243256,
29	87.5	7.5	1127	16	US-10-437-963-140467 Sequence 140467,
30	86.5	7.4	221	15	US-10-282-122A-69103 Sequence 69103, A
31	86	7.3	803	16	US-10-437-963-132702 Sequence 132702,
32	85	7.2	305	15	US-10-369-493-1179 Sequence 1179, Ap
33	85	7.2	766	14	US-10-317-832-120 Sequence 120, App
34	84.5	7.2	326	15	US-10-282-122A-56065 Sequence 56065, A
35	84	7.1	1040	16	US-10-437-963-140470 Sequence 140470,
36	83	7.1	253	15	US-10-282-122A-77898 Sequence 77898, A
37	82.5	7.0	272	15	US-10-282-122A-77471 Sequence 77471, A
38	82.5	7.0	638	16	US-10-437-963-185382 Sequence 185382,
39	82	7.0	218	15	US-10-415-554-2 Sequence 2, Appl
40	82	7.0	239	16	US-10-767-701-39668 Sequence 39668, A
41	82	7.0	447	15	US-10-335-977-9671 Sequence 9671, Ap
42	81.5	6.9	198	15	US-10-282-122A-50258 Sequence 50258, A
43	81.5	6.9	260	16	US-10-408-765A-1756 Sequence 1756, Ap
44	81.5	6.9	307	16	US-10-767-701-41868 Sequence 41868, A
45	81.5	6.9	320	16	US-10-437-963-201944 Sequence 201944,

ALIGNMENTS

RESULT 1
US-09-727-578-24
Sequence 24, Application US/09727578
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09727, 578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975, 698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-09-727-578-24

Query Match 100.0%; Score 1173; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTTERGK 60
DB 21 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTTERGK 80
QY 61 LAEADANLSAGVANAFSAFSGPITEKAPOLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEADANLSAGVANAFSAFSGPITEKAPOLHKLITNMIEDAGDLATRSAREKYMIR 140
QY 121 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNPOKNEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNPOKNEILKRGYELGES 200
QY 181 RVICGYHMOSVDVDAARIYGSANVATLTHTNPAFQOOLQKADFEAKTQK 228
DB 201 RVICGYHMOSVDVDAARIYGSANVATLTHTNPAFQOOLQKADFEAKTQK 248

RESULT 2

US-09-727-578-26
Sequence 26, Application US/09727578
Publication No. US2002004590A1

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-09-727-578-26

Query Match 96.8%; Score 1136; DB 9; Length 248;
Best Local Similarity 96.9%; Pred. No. 2.1e-109;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTTERGK 60
DB 21 LVPAQNDATTKPDLYLYKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRNTTERGK 80
QY 61 LAEADANLSAGVANAFSAFSGPITEKAPOLHKLITNMIEDAGDLATRSAREKYMIR 120
DB 81 LAEADANLSAGVANAFSAFSGPITEKAPOLHKLITNMIEDAGDLATRSAREKYMIR 140
QY 121 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNPOKNEILKRGYELGES 180
DB 141 PFAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELNPOKNEILKRGYELGES 200
QY 181 RVICGYHMOSVDVDAARIYGSANVATLTHTNPAFQOOLQKADFEAKTQK 228
DB 201 RVICGYHMOSVDVDAARIYGSANVATLTHTNPAFQOOLQKADFEAKTQK 248

RESULT 3

US-09-727-578-8
Sequence 8, Application US/09727578
Publication No. US2002004590A1

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-8

Query Match 93.0%; Score 1091; DB 9; Length 231;
Best Local Similarity 92.1%; Pred. No. 9 1e-105; Indels 0; Gaps 0;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYLLKNAQAIDSLALLPPPEVGSIAFLINDQAMTEKGLLRNTERGK 60
DB 3 LVATGNDTTPKPDLYLLKNSAINSLLALPPPAVGSIAFLINDQAMTEKGLLRNTERGK 62
QY 61 LAEDANLSAGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 120
DB 63 LAEDANLSGGVANAFSGAFSGPITEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 122
QY 121 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELINPORONEILKRGYELGQS 180
DB 123 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELINPORONEILKRGYELGQS 182
QY 181 RVICGYHMQSDVDARIVGSANVATLTNPAFOOOLQAKAEFAQHOK 228
DB 183 RVICGYHMQSDVDARIVGSANVATLTNPAFOOOLQAKAEFAQHOK 230

RESULT 4
US-09-727-578-7
Sequence 7, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-7

Query Match 93.0%; Score 1091; DB 9; Length 249;
Best Local Similarity 92.1%; Pred. No. 1e-104; Indels 0; Gaps 0;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYLLKNAQAIDSLALLPPPEVGSIAFLINDQAMTEKGLLRNTERGK 60
DB 21 LVATGNDTTPKPDLYLLKNSAINSLLALPPPAVGSIAFLINDQAMTEKGLLRNTERGK 80
QY 61 LAEDANLSAGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 120
DB 81 LAEDANLSGGVANAFSGAFSGPITEKDAPOHLKLTNMIEDAGDLATRSKAKHYMRIR 140
QY 121 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELINPORONEILKRGYELGQS 180
DB 141 PPAFGVSTCNTTEODKLSKSGSPSGHTSIGMATLVLAELINPORONEILKRGYELGQS 200
QY 181 RVICGYHMQSDVDARIVGSANVATLTNPAFOOOLQAKAEFAQHOK 228
DB 201 RVICGYHMQSDVDARIVGSANVATLTNPAFOOOLQAKAEFAQHOK 248

RESULT 5
US-09-727-578-22
Sequence 22, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Providencia stuartii
STRAIN: ATCC 29851
US-09-727-578-22

Query Match	88.2%	Score 1035	DB 9	Length 248
Best Local Similarity	85.5%	Pred. No. 6	7e-99	
Matches	194	Conservative	20	Mismatches 13; Indels 0; Gaps 0

QY	2	VPAGDATTKPDLYLYIKNAQAIIDSLALLPPPEVGSIAFLNDQAMYEKRLRLNTERGKL	61
Db	22	IPPGDVTYTKPDLYLYIKNSQAIDSLALLPPPEVGSILFLNDQAMYEKRLRLNTERGQ	81
QY	62	AAEDANTLSAGSYANAFSSAFSGPIETEKAPOLKLTLMNTIEPAGLARSAEAKYMRIRP	121
Db	82	AAKDADLAAAGYANAFSEAFSGPIETEKAPPELHKLTLMNTIEPAGLARSAEAKYMRIRP	141
QY	122	PAFYGVSTCNTTEODKLSKNSGSPSGHSTSIGWATLVIAEINPORNEILKKGYELGESR	181
Db	142	PAFYGVATCNTKDDOKLSKNSGSPSGHATLVIGWASLVLEIPEHQDKILKRGYELGGR	201
QY	182	VICGHWOSDVAARIVGSAAVATLHTNPAPOOQOKAKDEFAKTKQK	228
Db	202	VICGHWOSDVAARIVASGAVALTHSPERKQOKQAKDEFAKTKK	248

RESULT 6

```

1? Sequence 4, Application US/09727578
2Publication No. US20020004590A1
3
4GENERAL INFORMATION:
5
6APPLICANT: MIHARA, YASUHIRO
7APPLICANT: UTAGAWA, TAKASHI
8APPLICANT: YAMADA, HIDEAKI
9APPLICANT: ASANO, YASUHIKA
10TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
11TITLE OF INVENTION: ESTER
12NUMBER OF SEQUENCES: 30
13
14CORRESPONDENCE ADDRESS:
15
16ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
17STREET: 1155 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
18CITY: ARLINGTON
19STATE: VIRGINIA
20COUNTRY: USA
21
22ZIP: 22202
23
24COMPUTER READABLE FORM:
25
26MEDIUM TYPE: floppy disk
27
28COMPUTER: IBM PC compatible
29OPERATING SYSTEM: PC-DOS/MS-DOS
30SOFTWARE: PatentIn Release #1.0, Version #1.30
31
32CURRENT APPLICATION DATA:
33
34APPLICATION NUMBER: US/09/727,578
35
36FILING DATE:
37
38CLASSIFICATION:
39
40PRIOR APPLICATION DATA:
41
42APPLICATION NUMBER: 08/975,698
43
44FILING DATE:
45
46ATTORNEY/AGENT INFORMATION:
47
48NAME: OBLON, NORMAN F
49REGISTRATION NUMBER: 24,618
50REFERENCE/DOCKET NUMBER: 0010-0885-0
51
52TELECOMMUNICATION INFORMATION:
53
54TELEPHONE: (703) 413-3000
55
56TELEFAX: (703) 413-2220
57
58INFORMATION FOR SEQ ID NO: 4:
59
60SEQUENCE CHARACTERISTICS:
61
62LENGTH: 229 amino acids
63
64TYPE: amino acid
65
66TOPOLOGY: linear
67
68MOLECULE TYPE: protein
69
70ORIGINAL SOURCE:
71
72ORGANISM: Morganella morganii
73
74STRAIN: NCIMB 10466
75
76IS-09-727-578-4

```

Query Match	83.8%;	Score 983.5;	DB 9;	Length 229;
Best Local Similarity	82.9%;	Pred. No. 1.3e-93;		

	Matches	189;	Conservative	16;	Mismatches	22;	Indels	1;	Gaps	1
QY	2	VAGNDATKRP	LYLKNQAQ	DISLALLP	PRPVGSIA	FINDQAM	TEYEGRLIR	TERGKL	61	
		:	:	:	:	:	:	:	:	
Db	2	IPGNDATTKRP	LYLKNQ	QALDISKLLP	PRPVGSIO	FINDQAM	TEYEGRLIR	TERGKQ	61	
QY	62	AAEDANLSG	AVANAFSS	AFSGSPITEK	DAPQ	HLKLTNM	IEDAGL	ATRSAREK	MYRIRP	121
		:	:	:	:	:	:	:	:	
Db	62	AQADADLA	AGVATAF	SFGAFGYP	PIREKOSPE	LYKLLTM	IEDAGL	ATRSAREK	MYRIRP	121
QY	122	FAFYGVST	CTNTTEQ	DKLSKNGS	YPSGHTS	IGMATA	LVIABIN	FORONE	ILRGYELGSR	181
		:	:	:	:	:	:	:	:	
Db	122	FAFYGTCT	CKTKDQ	KLSSTNGS	YPSGHTS	IGMATA	LVIABIN	PAQADIL	IRGYQLGGR	181
QY	182	VICGSHM	QSDVDA	RIIVGS	AVVATL	HTNPA	FOQL	QRKDKFA	-KTKQ	228
		:	:	:	:	:	:	:	:	
Db	182	VICGSHM	QSDVDA	RIIVGS	AAVATL	HTSDPA	FOQL	QRKDKFO	SAQDSK	229

RESULT 7

Sequence 3 Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0865-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Morganella morganii
STRAIN: NCIMB 10466
US-09-727-578-3

Query Match 83.8% Score 983.5; DB 9, length 249;
 Best Local Similarity 82.9%; Pred. No. 1.5e-93;
 Matches 189; Conservative 16; Mismatches 22; Indels 1;
 Gaps 1.
 2 VPAGDATTGKDYLLKNAQAIDSLALPPPEVGSIAFLNQAMERKGLRLNRTGKLT. 61

```

Db      :|||||
22 IPAGDATTKPDLYLTKNOQAIDSLKLPPEVSGISQFLNDQAMYEKGRMLRTERGKQ 81
Qy      62 AAEDANLSAGGVANAFFSAGFSPITEKDAPOHLKLTNNIEDAGDLATRSAXEKMIRP 121
Db      82 AOADADLAAGVATAFSGAFGYPIREKOSPELYKLTNNIEDAGDLATRSAXEHYMRIRP 141
Qy      122 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNFORONEILKRGYELGESR 181
Db      142 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNFORONEILKRGYELGESR 201
Qy      182 VICGHWOSDVAARIIVGSAVVATLHTNPAFOOQLOKAKDEFA-KTOK 228
Db      202 VICGHWOSDVAARIIVGSAVVATLHTNPAFOOQLOKAKDEFA-KTOK 249

```

```

RESULT 8
US-10-220-481-116
; Sequence 116, Application US/10220481
; Publication No. US20040110670A1
; GENERAL INFORMATION:
; APPLICANT: ARICO, Maria B., et al.
; TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
; FILE REFERENCE: CHIR-15883/01US
; CURRENT APPLICATION NUMBER: US/10/220,481
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/IB01/00452
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 633
; SOFTWARE: SeqMan99, version 1.02
; SEQ ID NO 116
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel protein
US-10-220-481-116

```

```

Query Match      83.8%; Score 983.5; DB 16; Length 249;
Best Local Similarity 82.9%; Pred. No. 1.5e-93;
Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;
Qy      2 VPAGNDATTKPDLYLTKNOQAIDSLKLPPEVSGISQFLNDQAMYEKGRMLRTERGK 61
Db      22 IPAGDATTKPDLYLTKNOQAIDSLKLPPEVSGISQFLNDQAMYEKGRMLRTERGKQ 81
Qy      62 AAEDANLSAGGVANAFFSAGFSPITEKDAPOHLKLTNNIEDAGDLATRSAXEKMIRP 121
Db      82 AOADADLAAGVATAFSGAFGYPIREKOSPELYKLTNNIEDAGDLATRSAXEHYMRIRP 141
Qy      122 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNFORONEILKRGYELGESR 181
Db      142 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNFORONEILKRGYELGESR 201
Qy      182 VICGHWOSDVAARIIVGSAVVATLHTNPAFOOQLOKAKDEFA-KTOK 228
Db      202 VICGHWOSDVAARIIVGSAVVATLHTNPAFOOQLOKAKDEFA-KTOK 249

```

```

RESULT 9
US-09-727-578-28
; Sequence 28, Application US/09727578
; Publication No. US20020004590A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAHARA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

```

```

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Serratia ficaria
STRAIN: IAM 13540
US-09-727-578-28

```

```

Query Match      65.8%; Score 772; DB 9; Length 244;
Best Local Similarity 64.9%; Pred. No. 1.4e-71;
Matches 146; Conservative 31; Mismatches 48; Indels 0; Gaps 0;
Qy      4 AGNDATTKPDLYLTKNOQAIDSLKLPPEVSGISQFLNDQAMYEKGRMLRTERGK 63
Db      20 AAKVTTTPEVYFLOESQSIDSLKLPPEVSGISQFLNDQAMYEKGRMLRTERGKQ 79
Qy      64 EDANLSAGGVANAFFSAGFSPITEKDAPOHLKLTNNIEDAGDLATRSAXEKMIRPFA 123
Db      80 DDAHAGGVANAFFSAGFSPITEKDAPOHLKLTNNIEDAGDLATRSAXEHYMRIRPFA 139
Qy      124 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNFORONEILKRGYELGESR 183
Db      140 FAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNFORONEILKRGYELGESR 201
Qy      184 VICGHWOSDVAARIIVGSAVVATLHTNPAFOOQLOKAKDEFA-KTOK 228
Db      200 VICGHWOSDVAARIIVGSAVVATLHTNPAFOOQLOKAKDEFA-KTOK 244

```

```

RESULT 10
US-09-738-626-4817
; Sequence 4817, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125

```

CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4817
LENGTH: 622
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4817

Query Match 11.3%; Score 133; DB 9; Length 622;
Best Local Similarity 26.6%; Pred. No. 0.00014;
Matches 41; Conservative 23; Mismatches 60; Indels 30; Gaps 4;

99 NMIEDAGDL-----ATRSACEKYMRIIRPPAF-----YGVST---C 130
173 NMAETGELGSLTYDLIAIRQHATSNNAKAYIQYRPPIKMTESIEPEAMGSGVDMPEYA 232
QY 131 NTEED--KLSKNGSYPSGHTSIGMATVLAELINPORNELIKRGYELGSGRVIGYHM 188
DB 233 NPLRKDESEAMASDGGFPGHTSAGMATNGLAAYAPQYQDKLMTAAEIGESRIQLGMS 292
QY 189 QSDVDARIYGSVAVVATLHTNPAFQQQLKAKDE 222
DB 293 PLDVGIGRVLTATITGALNDPVLDSVKAAPDD 326

RESULT 11
US-10-437-963-165801
Sequence 165801, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437, 963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 165801
LENGTH: 414
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_64572C.1.pcp
US-10-437-963-165801

Query Match 9.0%; Score 105; DB 16; Length 414;
Best Local Similarity 28.8%; Pred. No. 0.062;
Matches 45; Conservative 22; Mismatches 59; Indels 30; Gaps 7;

QY 22 AIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERG-KLAABDANLSAGGVANA--- 76
DB 84 AMKHVALAPPPSPKSKKSKNSVWTR-----PNSRKKGKAKQPAVALAGSGANGRL 139
QY 77 ---SSAGSGSPIT-----EKDAPQHLKLTNM-----IEDAGLATSAEKYMRI 119
DB 140 PKPSSGDELVLVTAPRAAERNDAPDLPVLLSVFESKSDYEVSDRLTAGSTKGYRMV 199
QY 120 RPAFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGMAT 155

DB 200 R--ATRGVAAGAMFEVKVHLGS--TGHTRLGWAT 231

RESULT 12
US-09-727-578-1
Sequence 1, Application US/09727578
Publication No. US20020004590A1
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727, 578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Morganella morganii
STRAIN: NCIMB 10466
US-09-727-578-1

Query Match 8.3%; Score 97; DB 9; Length 20;
Best Local Similarity 94.4%; Pred. No. 0.0055;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPAGNDATTKPDLYLKN 19
DB 2 IPAGNDATTKPDLYLKN 19
RESULT 13
US-10-437-963-112291
Sequence 112291, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei

[illegible]

Db	269 A---AQAKDITLEKGGQ-----GYAVTKDT---ISSAKTASEKTAPV----AEKA 309
Qy	220 KD 221
Db	310 KD 311

Search completed: March 2, 2005, 20:44:03
Job time : 87.4314 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:16:41 ; Search time 29.8039 Seconds
(without alignments)
571.065 Million cell updates/sec

Title: US-09-807-990a-125
Perfect score: 1173
Sequence: 1 LVPAQNDAATKPDLYLKNA.....NPAFOQLQKAKDEPAKTQK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173	100.0	248	US-08-750-145A-20	Sequence 20, Appl
2	1173	100.0	248	US-08-975-698A-24	Sequence 24, Appl
3	1173	100.0	248	US-09-417-090-24	Sequence 24, Appl
4	1173	100.0	248	US-09-727-578-24	Sequence 24, Appl
5	1139	97.1	253	US-09-489-039A-7933	Sequence 7933, Ap
6	1136	96.8	248	US-08-750-145A-22	Sequence 22, Appl
7	1136	96.8	248	US-08-975-698A-26	Sequence 26, Appl
8	1136	96.8	248	US-09-417-090-26	Sequence 26, Appl
9	1136	96.8	248	US-09-727-578-26	Sequence 26, Appl
10	1091	93.0	231	US-08-750-145A-11	Sequence 11, Appl
11	1091	93.0	231	US-08-975-698A-8	Sequence 8, Appl
12	1091	93.0	231	US-09-417-090-8	Sequence 8, Appl
13	1091	93.0	231	US-09-727-578-8	Sequence 8, Appl
14	1091	93.0	249	US-08-750-145A-10	Sequence 10, Appl
15	1091	93.0	249	US-08-975-698A-7	Sequence 7, Appl
16	1091	93.0	249	US-09-417-090-7	Sequence 7, Appl
17	1091	93.0	249	US-09-727-578-7	Sequence 7, Appl
18	1035	88.2	248	US-08-750-145A-18	Sequence 18, Appl
19	1035	88.2	248	US-08-975-698A-22	Sequence 22, Appl
20	1035	88.2	248	US-09-417-090-22	Sequence 22, Appl
21	1035	88.2	248	US-09-727-578-22	Sequence 22, Appl
22	983.5	83.8	229	US-08-750-145A-4	Sequence 4, Appl
23	983.5	83.8	229	US-08-975-698A-4	Sequence 4, Appl
24	983.5	83.8	229	US-09-417-090-4	Sequence 4, Appl
25	983.5	83.8	229	US-09-727-578-4	Sequence 4, Appl
26	983.5	83.8	249	US-08-750-145A-3	Sequence 3, Appl
27	983.5	83.8	249	US-08-975-698A-3	Sequence 3, Appl

28	983.5	83.8	249	US-09-417-090-3	Sequence 3, Appl
29	983.5	83.8	249	US-09-727-578-3	Sequence 3, Appl
30	772	65.8	244	US-08-750-145A-24	Sequence 24, Appl
31	772	65.8	244	US-08-975-698A-28	Sequence 28, Appl
32	772	65.8	244	US-09-417-090-28	Sequence 28, Appl
33	772	65.8	244	US-09-727-578-28	Sequence 28, Appl
34	317	27.0	252	US-07-717-332D-2	Sequence 2, Appl
35	193.5	16.5	943	US-09-540-236-3458	Sequence 3458, Ap
36	191.5	16.3	428	US-09-489-039A-10941	Sequence 10941, A
37	166	14.2	253	US-09-252-991A-28557	Sequence 28557, A
38	153	13.0	987	US-09-543-681A-7785	Sequence 7785, Ap
39	97	8.3	20	US-08-750-145A-1	Sequence 1, Appl
40	97	8.3	20	US-08-975-698A-1	Sequence 1, Appl
41	97	8.3	20	US-09-417-090-1	Sequence 1, Appl
42	97	8.3	20	US-09-727-578-1	Sequence 1, Appl
43	92.5	7.9	187	US-09-328-352-7918	Sequence 7918, Ap
44	92	7.8	159	US-09-602-787A-102	Sequence 102, App
45	90.5	7.7	244	US-09-543-681A-4595	Sequence 4595, Ap

ALIGNMENTS

RESULT: 1
US-08-750-145A-20
Sequence 20, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
PHOSPHATE Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUGSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750, 145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010

US-08-750-145A-20

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERCK 60
DB 21 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERCK 80
QY 61 LAADANLSAGGVANNAFSSAFSGSPITEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 120
DB 81 LAADANLSAGGVANNAFSSAFSGSPITEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 140
QY 121 PPAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPNORNEILKRGYELGES 180
DB 141 PPAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPNORNEILKRGYELGES 200
QY 181 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFOOQLQAKDEFAKTOK 228
DB 201 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFOOQLQAKDEFAKTOK 248

RESULT 2

US-08-975-698A-24
Sequence 24, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
US-08-975-698A-24

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERCK 60
DB 21 LVPAGNDATTKPDLYYLKNAQAIDSLALLPPEPEVGSIAFLNDQAMYEKGRLLRNTERCK 80
QY 61 LAADANLSAGGVANNAFSSAFSGSPITEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 120
DB 81 LAADANLSAGGVANNAFSSAFSGSPITEKDAPOHLKLTNMI EDAGDLATRSKKEKYMIR 140
QY 121 PPAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPNORNEILKRGYELGES 180
DB 141 PPAFYGVSTCNTTEEDDKLSKNGSYSGHTSIGMATLVLAELNPNORNEILKRGYELGES 200
QY 181 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFOOQLQAKDEFAKTOK 228
DB 201 RVICGYHWSQDVDAARIVGSAVVATLHTNPAFOOQLQAKDEFAKTOK 248

RESULT 3

US-09-417-090-24
Sequence 24, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-OCT-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
SEQUENCE DESCRIPTION: SEQ ID NO: 24
US-09-417-090-24

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LVPAGNDATTTPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRTERGK 80
Qy 61 LAEDANISAGVANAFSSAFSGSPITEKDAPOQLHKLNTNMTEDAGDLATRSACEKYMIR 120
Db 81 LAEDANISAGVANAFSSAFSGSPITEKDAPOQLHKLNTNMTEDAGDLATRSACEKYMIR 140
Qy 121 PFAPYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
Db 141 PFAPYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 200
Qy 181 RVICGYHMQSDVDAAIRIVGSAVAVATLHTNPAFOOOLQAKDEFAKTOK 228
Db 201 RVICGYHMQSDVDAAIRIVGSAVAVATLHTNPAFOOOLQAKDEFAKTOK 248

RESULT 4

US-09-727-578-24
; Sequence 24, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727, 578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975, 698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24, 618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
; US-09-727-578-24

Query Match 100.0%; Score 1173; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 1,86-127;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LVPAGNDATTTPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRTERGK 60
Db 21 LVPAGNDATTTPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRTERGK 80
Qy 61 LAEDANISAGVANAFSSAFSGSPITEKDAPOQLHKLNTNMTEDAGDLATRSACEKYMIR 120

Db 81 LAEDANISAGVANAFSSAFSGSPITEKDAPOQLHKLNTNMTEDAGDLATRSACEKYMIR 140
Qy 121 PFAPYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
Db 141 PFAPYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 200
Qy 181 RVICGYHMQSDVDAAIRIVGSAVAVATLHTNPAFOOOLQAKDEFAKTOK 228
Db 201 RVICGYHMQSDVDAAIRIVGSAVAVATLHTNPAFOOOLQAKDEFAKTOK 248

RESULT 5

US-09-489-039A-7933
; Sequence 7933, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7933
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7933

Query Match 97.1%; Score 1139; DB 4; Length 253;
Best Local Similarity 96.9%; Pred. No. 1,76-123;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 LVPAGNDATTTPDLYLKNQAIDSLALLPPPEVGSIAFLNDQAMYEKRLRTERGK 60
Db 26 LVPAGNDATTTPDLYLKNQAIDSLALLPPPAVGSIAFLNDQAMYEKRLRTERGK 85
Qy 61 LAEDANISAGVANAFSSAFSGSPITEKDAPOQLHKLNTNMTEDAGDLATRSACEKYMIR 120
Db 86 LAEDANISAGVANAFSSAFSGSPITEKDAPOQLHKLNTNMTEDAGDLATRSACEKYMIR 145
Qy 121 PFAPYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
Db 146 PFAPYGVSTCMTTEODKLSKNGSPSGHTSIGMATLVLAELINPORONEILKRGYELGES 205
Qy 181 RVICGYHMQSDVDAAIRIVGSAVAVATLHTNPAFOOOLQAKDEFAKTOK 228
Db 206 RVICGYHMQSDVDAAIRIVGSAVAVATLHTNPAFOOOLQAKDEFAKTOK 253

RESULT 6

US-08-750-145A-22
; Sequence 22, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: UTAGAWA, Takashi
; APPLICANT: YAMADA, Hideaki
; APPLICANT: ASANO, Yasuhisa
; TITLE OF INVENTION: Method for Producing Nucleoside-5'-
; TITLE OF INVENTION: Phosphate Ester
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P. C.
; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-3000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-750-145A-22

Query Match 96.8%; Score 1136; DB 3; Length 248;
Best Local Similarity 96.9%; Pred. No. 3 6e-123;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 LVPAAGDATTTPDLYLKNAQAIIDSLALLPPPEVGSIAFLNDQAMYEKRLLRTERGK 60
DB 21 LVPAAGDATTTPDLYLKNAQAIIDSLALLPPPEVGSIAFLNDQAMYEKRLLRTERGK 80
QY 61 LAEDANLSAGGVANNAFSAFSGSPITEKDAPOHLKLTNNMIEDAGDLATRSAREKRYR 120
DB 81 LAEDANLSAGGVANNAFSAFSGSPITEKDAPOHLKLTNNMIEDAGDLATRSAREKRYR 140
QY 121 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELNPOQNEILKRGYELGES 180
DB 141 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELNPOQNEILKRGYELGES 200
QY 181 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOQOLQAKDEFKAKOK 228
DB 201 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOQOLQAKDEFKAKOK 248

RESULT 7
US-08-975-698A-26
Sequence 26, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-3000
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-975-698A-26

Query Match 96.8%; Score 1136; DB 3; Length 248;
Best Local Similarity 96.9%; Pred. No. 3 6e-123;
Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 LVPAAGDATTTPDLYLKNAQAIIDSLALLPPPEVGSIAFLNDQAMYEKRLLRTERGK 60
DB 21 LVPAAGDATTTPDLYLKNAQAIIDSLALLPPPEVGSIAFLNDQAMYEKRLLRTERGK 80
QY 61 LAEDANLSAGGVANNAFSAFSGSPITEKDAPOHLKLTNNMIEDAGDLATRSAREKRYR 120
DB 81 LAEDANLSAGGVANNAFSAFSGSPITEKDAPOHLKLTNNMIEDAGDLATRSAREKRYR 140
QY 121 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELNPOQNEILKRGYELGES 180
DB 141 PFAFYGVSTCTTTEODKLSKNGSYPSGHTSIGMATLVLAELNPOQNEILKRGYELGES 200
QY 181 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOQOLQAKDEFKAKOK 228
DB 201 RVICGYHMOSDVDAARIVGSAVVAATLHTNPAFOQOLQAKDEFKAKOK 248

RESULT 8
US-09-417-090-26
Sequence 26, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/417,090

FILING DATE: 13-Oct-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975,698
 FILING DATE: 21-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Klebsiella planticola
 STRAIN: IFO 14939
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 US-09-417-090-26

Query Match 96.8%; Score 1136; DB 3; Length 248;
 Best Local Similarity 96.9%; Pred. No. 3.6e-123;
 Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
 DB 21 LVPAGNDATTKPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 80
 QY 61 LAADANLSAGVANAFSAFSGSPITEKDAFQHLKLTNMTEDAGDLATRSAGEKYMIR 120
 DB 81 LAADANLSAGVANAFSAFSGSPITEKDAFQHLKLTNMTEDAGDLATRSAGEKYMIR 140
 QY 121 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 180
 DB 141 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 200
 QY 181 RVICGYHQSVDVDAARIYGSAAVATLTNPAFQOOLQAKDEFKAKO 228
 DB 201 RVICGYHQSVDVDAARIYGSAAVATLTNPAFQOOLQAKDEFKAKO 248

RESULT 9
 US-09-727-578-26
 Sequence 26, Application US/09727578
 Patent No. 6355472
 GENERAL INFORMATION:
 APPLICANT: MIHARA, YASUHIRO
 APPLICANT: UTAGAWA, TAKASHI
 APPLICANT: YAMADA, HIDEAKI
 APPLICANT: ASANO, YASUHISA
 TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/727,578
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/975,698
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0885-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Klebsiella planticola
 STRAIN: IFO 14939
 US-09-727-578-26

Query Match 96.8%; Score 1136; DB 3; Length 248;
 Best Local Similarity 96.9%; Pred. No. 3.6e-123;
 Matches 221; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 60
 DB 21 LVPAGNDATTKPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMYEKGRLLRTERGK 80
 QY 61 LAADANLSAGVANAFSAFSGSPITEKDAFQHLKLTNMTEDAGDLATRSAGEKYMIR 120
 DB 81 LAADANLSAGVANAFSAFSGSPITEKDAFQHLKLTNMTEDAGDLATRSAGEKYMIR 140
 QY 121 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 180
 DB 141 PFAFYGVSTCMTTEODKLSKNGSYPSGHTSIGMATLVLAETINPORONEILKRGYELGES 200
 QY 181 RVICGYHQSVDVDAARIYGSAAVATLTNPAFQOOLQAKDEFKAKO 228
 DB 201 RVICGYHQSVDVDAARIYGSAAVATLTNPAFQOOLQAKDEFKAKO 248

RESULT 10
 US-08-750-145A-11
 Sequence 11, Application US/08750145A
 Patent No. 6010851
 GENERAL INFORMATION:
 APPLICANT: MIHARA, Yasuhiro
 APPLICANT: UTAGAWA, Takashi
 APPLICANT: YAMADA, Hideaki
 APPLICANT: ASANO, Yasuhisa
 TITLE OF INVENTION: Method for Producing Nucleoside-5'-
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/750,145A
 FILING DATE: 01-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-149781
 FILING DATE: 05-May-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Escherichia blattae
STRAIN: JCM 1650
US-08-750-145A-11

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5.3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLNTERGK 60
DB 3 LVATGNDTTPKPDLYYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEKRLNTERGK 62
QY 61 LAEDANLSAGVANAFAFGSPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 120
DB 63 LAEDANLSAGVANAFAFGSPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 122
QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAINEPQONEILKRGYELGS 180
DB 123 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAINEPQONEILKRGYELGS 182
QY 181 RVICGYHMOVDVDAARIYGSAAVATLHTNPAFOOQLOKAKDEFKTKT 228
DB 183 RVICGYHMOVDVDAARIYGSAAVATLHTNPAFOOQLOKAKDEFKTKT 230

RESULT 11

US-08-975-698A-8
Sequence 8, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Escherichia blattae
STRAIN: JCM 1650
US-08-975-698A-8

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5.3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAGNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLNTERGK 60
DB 3 LVATGNDTTPKPDLYYLKNSSEAINSLALPPPAVGSIAFLNDQAMYEKRLNTERGK 62
QY 61 LAEDANLSAGVANAFAFGSPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 120
DB 63 LAEDANLSAGVANAFAFGSPITEKAPALHKLNTMTEDAGDLATRSAREKMYRIR 122
QY 121 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAINEPQONEILKRGYELGS 180
DB 123 PFAFYGVSTCNTTEODKLSKNGSPSGHTSIGMATLVLAINEPQONEILKRGYELGS 182
QY 181 RVICGYHMOVDVDAARIYGSAAVATLHTNPAFOOQLOKAKDEFKTKT 228
DB 183 RVICGYHMOVDVDAARIYGSAAVATLHTNPAFOOQLOKAKDEFKTKT 230

RESULT 12

US-09-417-090-8
Sequence 8, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-417-090-8

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5,3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
DB 3 LVATGNDTTTKPDLYLLKNSBAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTERGK 62
QY 61 LAEPDANISAGVANAFAFGSPITTEKDAFOLHKLITNMIEDAGDLATRSKAKHYMRIR 120
DB 63 LAEPDANISAGVANAFAFGSPITTEKDAFOLHKLITNMIEDAGDLATRSKAKHYMRIR 122
QY 121 PPAFYGVSTCWTTEQDKLSKNGSYSPSGHTSIGMATLVLAELNIPORONEILKRGYELGS 180
DB 123 PPAFYGVSTCWTTEQDKLSKNGSYSPSGHTSIGMATLVLAELNIPORONEILKRGYELGS 182
QY 181 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKTOK 228
DB 183 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKTOK 230

RESULT 13
US-09-727-578-8
Sequence 8, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/727,578
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-09-727-578-8

Query Match 93.0%; Score 1091; DB 3; Length 231;
Best Local Similarity 92.1%; Pred. No. 5,3e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYLLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKGRLLRNTERGK 60
DB 3 LVATGNDTTTKPDLYLLKNSBAINSLALPPPAVGSIAFLNDQAMYEGRLLRNTERGK 62
QY 61 LAEPDANISAGVANAFAFGSPITTEKDAFOLHKLITNMIEDAGDLATRSKAKHYMRIR 120
DB 63 LAEPDANISAGVANAFAFGSPITTEKDAFOLHKLITNMIEDAGDLATRSKAKHYMRIR 122
QY 121 PPAFYGVSTCWTTEQDKLSKNGSYSPSGHTSIGMATLVLAELNIPORONEILKRGYELGS 180
DB 123 PPAFYGVSTCWTTEQDKLSKNGSYSPSGHTSIGMATLVLAELNIPORONEILKRGYELGS 182
QY 181 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKTOK 228
DB 183 RVICGYHMQSDVDARIVGSAVVATLHTNPAFQOOLQAKADEFAKTOK 230

RESULT 14
US-08-750-145A-10
Sequence 10, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/750,145A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Escherichia blattae
STRAIN: JCM 1650
US-08-750-145A-10

Query Match 93.0%; Score 1091; DB 3; Length 249;
Best Local Similarity 92.1%; Pred. No. 5.9e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRTERGK 60
DB 21 LVATGNDTTTKPDLYYLKNSAINSLLPPPAVGSIAFLNDQAMYEKRLRTERGK 80
QY 61 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 120
DB 81 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 140
QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
DB 141 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGES 200
QY 181 RVICGYHMQSDVDARIVGSAVVATLTNPAFOOQLOKAKDEFAPKQK 228
DB 201 RVICGYHMQSDVDARIVGSAVVATLTNPAFOOQLOKAKDEFAPKQK 248

RESULT 15
US-08-975-698A-7
Sequence 7, Application US/08975698A
Patent No. 6015697

GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,698A
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Escherichia blattae
STRAIN: JCM 1650
US-08-975-698A-7

Query Match 93.0%; Score 1091; DB 3; Length 249;
Best Local Similarity 92.1%; Pred. No. 5.9e-118;
Matches 210; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 LVPAQNDATTKPDLYYLKNAQAIDSLALPPPEVGSIAFLNDQAMYEKRLRTERGK 60
DB 21 LVATGNDTTTKPDLYYLKNSAINSLLPPPAVGSIAFLNDQAMYEKRLRTERGK 80
QY 61 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 120
DB 81 LAEDANLSAGGVANAFSSAFSGSPITEKDAPOHLKLTNMIEDAGDLATRSADHYMRIR 140
QY 121 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGES 180
DB 141 PPAFYGVSTCNTTEBODKLSKNGSYPSGHTSIGMATLVLAELINPORONEILKRGYELGES 200
QY 181 RVICGYHMQSDVDARIVGSAVVATLTNPAFOOQLOKAKDEFAPKQK 228
DB 201 RVICGYHMQSDVDARIVGSAVVATLTNPAFOOQLOKAKDEFAPKQK 248

Search completed: March 2, 2005, 20:28:51
Job time: 30.8039 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 20:15:51 ; Search time 25.333 Seconds
(without alignments)
865.951 Million cell updates/sec

Title: US-09-807-990A-125

Perfect score: 1173

Sequence: 1 LVPAGNDATTKRPDIYYLKNA.....NPAFQQLQAKADEFAKTOK 228

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	88.2	248	1	PAOFCS acid phosphatase (
2	983.5	83.8	249	1	SI187 acid phosphatase (
3	483	41.2	250	1	A4130 acid phosphatase (
4	476.5	40.6	250	2	AF1025 acid phosphatase (
5	341.5	29.1	264	1	A3044 acid phosphatase (
6	274.5	23.4	258	2	E87293 acid phosphatase (
7	186	15.9	2314	2	T28698 acid phosphatase (
8	161	13.7	241	2	C83621 acid phosphatase (
9	151	12.9	591	2	C96991 acid phosphatase (
10	147	12.5	660	2	AB3118 acid phosphatase (
11	147	12.5	660	2	E98169 acid phosphatase (
12	105	9.0	145	2	F75447 acid phosphatase (
13	98.5	8.4	259	2	A87623 acid phosphatase (
14	96	8.2	178	2	D82070 acid phosphatase (
15	93.5	8.0	643	1	T07064 acid phosphatase (
16	92	7.8	217	2	D97672 acid phosphatase (
17	92	7.8	242	2	AB2897 acid phosphatase (
18	91.5	7.8	725	2	G90555 acid phosphatase (
19	90.5	7.7	562	2	G46281 acid phosphatase (
20	90	7.7	437	2	H81143 acid phosphatase (
21	89	7.6	608	2	D87912 acid phosphatase (
22	88.5	7.5	1707	2	S77910 acid phosphatase (
23	87	7.4	292	2	AF3647 acid phosphatase (
24	86	7.3	525	2	C82914 acid phosphatase (
25	85.5	7.3	514	2	A45228 acid phosphatase (
26	85	7.2	766	2	A24786 acid phosphatase (
27	84.5	7.2	921	2	A54139 acid phosphatase (
28	84.5	7.2	1261	2	T48096 acid phosphatase (
29	84	7.2	1588	2	A66036 acid phosphatase (

30	84	7.2	1588	2	H91188 probable adhesin E
31	84	7.2	3746	1	YGPLV3 alpha-aminoadipyl-L-
32	84	7.2	3791	1	YGPLV8 alpha-aminoadipyl-L-
33	83.5	7.1	320	2	AE2020 hypothetical prote
34	83.5	7.1	589	2	T29897 hypothetical prote
35	83	7.1	253	2	AB0271 phosphatidylglycer
36	83	7.1	493	2	PE0157 MDM10 protein - ye
37	83	7.1	753	2	S22802 transposase (clone
38	82.5	7.0	292	1	G82076 3',5'-cyclic-nucle
39	82.5	7.0	292	2	C65070 hypothetical prote
40	82.5	7.0	498	2	C87551 glutamyl-tRNA (Gln)
41	82.5	7.0	514	2	S60033 25-hydroxyvitamin
42	82.5	7.0	721	2	S31820 gene Mx protein -
43	82.5	7.0	721	2	A37472 interferon-inducib
44	82	7.0	202	2	A82076 conserved hypothet
45	82	7.0	218	2	B97497 22k outer membrane

ALIGNMENTS

RESULT 1

PAOFCS acid phosphatase (EC 3.1.3.2) - Providencia stuartii
C:Species: Providencia stuartii
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: S19888

R:Riccio, M.L., Lombardi, G., Chiesurin, A., Satta, G.
submitted to the EMBL Data Library, February 1992

A:Reference number: S19888

A:Accession: S19888

A:Molecule type: DNA

A:Residues: 1-248 <R1C>

A:Cross-references: UNIPROT:P26975; EMBL:X64820; NID:q45861; PIDN:CAA46032.1; PID:q45862

C:Genetics:

A:Gene: phoN

C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

C:Keywords: phosphoric monoster hydrolase.

P:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GN>

Query Match 88.2%; Score 1035; DB 1; Length 248;
Best Local Similarity 85.5%; Pred. No. 1.58-82;
Matches 194; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY	2	VPAQNDATTKRPDIYYLKNAQIDSLALPPPEVGSIAFLNDQMYEGRLLRNTREGKL	61
DB	22	IPPGNDVTTKPDLYLLKNSQALIDSLALPPPEVGSILFLNDQMYEGRLLRNTREGQ	81
QY	62	AAEDANLSAGGVANAFSSAFSGSPITTEKDAPOHLKLTNMIEDAGDLATRSKKEKYMRIIP	121
DB	82	AAKADLAAAGGVANAFSEAFGYPITTEKDAPEIHLKLTNMIEDAGDLATRSKKEKYMRIIP	141
QY	122	PAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATVLAELINPQRONEILRGYELGSR	181
DB	142	FAFYGVATCNTKQDDKLSKNGSYSGHTAIGMASVALVSEINPQRONEILRGYELGSR	201
QY	182	VICGYHWQSDVDARIVGSAVATLTNPAFOQLQAKADEFAKTOK	228
DB	202	VICGYHWQSDVDARIVASGAVATLTNPNFQKQAKADEFAKTOK	248

RESULT 2

SI9187 acid phosphatase (EC 3.1.3.2) - Morganella morganii
C:Species: Morganella morganii
C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 09-Jul-2004

C:Accession: S19187

R:Thaller, M.C.; Berluti, F.; Schippa, S.; Rosolini, G.M.
submitted to the EMBL Data Library, February 1992

A:Description: Sequencing the Morganella morganii phoC gene coding for a periplasmic ac

A:Reference number: S19187

A:Accession: S19187
A:Molecule type: DNA

A:Residues: 1-249 <THA>
 A:Cross-references: UNIPROT:P26581; EMBL:X64444; NID:944463; PIDN:CAA5774.1; PID:944464
 C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
 C:Keywords: phosphoric monoester hydrolase
 F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 83.8%; Score 983.5; DB 1; Length 249;
 Best Local Similarity 82.9%; Pred. No. 4,5e-78;
 Matches 189; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 2 VPAGNDATYTPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMEYKRLNTERGKL 61
 DB 22 IIPANDATYTPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMEYKRLNTERGKL 81
 QY 62 AADANASAGVANAFSAGSPITEKDAPOHLKLTNMIEDAGDLATRSKAKYKIRIP 121
 DB 82 AQDADADLAGGVATRSAGATGYPTTEKDSPELYKLTNMIEDAGDLATRSKAKYKIRIP 141
 QY 122 PAFYGVSTCCTTTEODKLSKNGSYPSGHTSIGMATLVLAEPORONELKRGYELGESR 181
 DB 142 FAFYGVSTCCTTTEODKLSKNGSYPSGHTSIGMATLVLAEPORONELKRGYELGESR 201
 QY 182 VICGYHMOVDVDAARIYVGSAAVATHTNPAFOOLAKADEFA-KTQK 228
 DB 202 VICGYHMOVDVDAARIYVGSAAVATHTNPAFOOLAKADEFA-KTQK 249

RESULT 3

A41330
 acid phosphatase (EC 3.1.3.2) Phos precursor - Salmonella typhimurium
 N:Alternate names: glycerophosphatase; nonspecific acid phosphatase; phosphomonoesterase
 C:Species: Salmonella typhimurium
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S20958; A41330; S14515; S18926
 R:Grossman, E.A.; Saier Jr., M.H.; Ochman, H.
 EMBL J. 11, 1309-1316, 1992
 A:Title: Horizontal transfer of a phosphatase gene as evidence for mosaic structure of t
 A:Reference number: S20958; MUID:92224869; PMID:1339343
 A:Accession: S20958
 A:Molecule type: DNA
 A:Residues: 1-250 <GRO>
 A:Cross-references: UNIPROT:P26976; EMBL:X63599; NID:947823; PIDN:CAA45144.1; PID:947824
 R:Kashihara, M.; Nakata, A.; Shingawa, H.
 J. Bacteriol. 173, 6760-6765, 1991
 A:Title: Molecular analysis of the Salmonella typhimurium phoN gene, which encodes nonsp
 A:Reference number: A41330; MUID:92041557; PMID:1938882
 A:Accession: A41330
 A:Molecule type: DNA
 A:Residues: 1-228, 'SVRS' <KAS>
 A:Cross-references: GB:X59036; NID:948894; PIDN:CAA11760.1; PID:948895
 C:Genetics:
 A:Gene: phoN
 A:Map position: 96 min
 A>Note: regulated by the two-component regulatory system consisting of phoP and phoQ
 C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
 C:Keywords: periplasmic space; phosphoric monoester hydrolase
 F:108-221/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 41.2%; Score 483; DB 1; Length 250;
 Best Local Similarity 47.0%; Pred. No. 1.6e-34;
 Matches 95; Conservative 33; Mismatches 74; Indels 0; Gaps 0;

QY 21 QAIDSLALPPPEVGSIAFLNDQAMEYKRLNTERGKLAAEDANISAGVANAFSSA 80
 DB 31 ESNVSGFLLPPPPGNDPARYYDEKAVFKGYAIAKGSFPMKQAAEDADVSENIARIFSPV 90
 QY 81 FGSPTTEKDAPOHLKLTNMIEDAGDLATRSKAKYKIRIPFAVYSTCCTTEODKLSK 140
 DB 91 VGAKINPDTEPTNMLKNLLTMGGYATASAKYKIRIPFVFNSTCRPEDENTLRK 150
 QY 141 NGSPSPGHTSIGMATLVLAEPORONELKRGYELGESRVICGYHMOVDVDAARIYVS 200
 DB 151 NGSPSPGHTSIGMATLVLAEPORONELKRGYELGESRVICGYHMOVDVDAARIYVS 210

QY 201 AVATLHTNPAFOOLAKADE 222
 DB 211 VEFARLQITIPAFQKSLAKVREE 232

RESULT 4

AF1025
 acid phosphatase (EC 3.1.3.2) - Salmonella enterica subsp. enterica serovar Typhi
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A>Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
 C:Accession: AF1025
 R:Parhill, D.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Mole, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF1025
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD09303.1; PID:916505305; GSPDB:GN00176
 C:Genetics:
 A:Gene: phoN
 C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
 C:Keywords: phosphoric monoester hydrolase

Query Match 40.6%; Score 476.5; DB 2; Length 250;
 Best Local Similarity 44.7%; Pred. No. 5.7e-34;
 Matches 96; Conservative 37; Mismatches 79; Indels 3; Gaps 1;

QY 8 ATTPDLYLKNQAQIDSLALPPPEVGSIAFLNDQAMEYKRLNTERGKLAAEDAN 67
 DB 21 ATMPQ---FSPSESVNSQFYLPPPPGNDPARYYDEKAVFKGYAIAKGSFPMKQAAEDAD 77
 QY 68 LSAAGVANAFSAGSPITEKDAPOHLKLTNMIEDAGDLATRSKAKYKIRIPFAVYGV 127
 DB 78 ISENIARIFSPVGAIAINPDTEPTNMLKNLLTMGGYATASAKYKIRIPFVFNH 137
 QY 128 STCCTTTEODKLSKNGSYPSGHTSIGMATLVLAEPORONELKRGYELGESRVICGYH 187
 DB 138 STCRPEDENTLRKDSGTPSGHTYATLVLSQAPPERQOELARRGMEFGSGRVICGAH 197
 QY 188 WQSDVDAARIYVGSAAVATHTNPAFOOLAKADE 222
 DB 198 WQSDVDAARIYVGSAAVATHTNPAFOOLAKADE 232

RESULT 5

A32044
 acid phosphatase (EC 3.1.3.2) - Zymomonas mobilis
 C:Species: Zymomonas mobilis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A32044
 R:Pond, J.L.; Eddy, C.K.; Mackenzie, K.F.; Conway, T.; Borecky, D.J.; Ingram, L.O.
 J. Bacteriol. 177, 767-774, 1989
 A:Title: Cloning, sequencing, and characterization of the principal acid phosphatase, the
 A:Reference number: A32044; MUID:89123152; PMID:2914872
 A:Accession: A32044
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <PON>
 A:Cross-references: UNIPROT:P14924; GB:M24141; NID:9155613; PIDN:AAA27700.1; PID:9155614
 C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
 C:Keywords: phosphoric monoester hydrolase
 F:99-212/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 29.1%; Score 341.5; DB 1; Length 264;
 Best Local Similarity 36.8%; Pred. No. 3.4e-22;
 Matches 75; Conservative 31; Mismatches 97; Indels 1; Gaps 1;

QY 24 DSIALLPPEVSGIAFLNDQAMYEKGRLLRNTBGRKLAEDANLSAGGVANAFSSAFGS 83
DB 44 DPLILAPPEPTSGSPLOAHDDOTFNSTROLKSTKALMTQDADHLAVALKDYACAAAM 103
QY 84 PITTEKADPOLHKLITNMIEDAGDLATRSAREKYMIRPPAFYGVSTCNTTEODKLSKNGS 143
DB 104 NLDIADLPHLANILKRALRTEYDDIGR-AKNNMNRKRPVDPDQPICTEKREGLGKGS 162
QY 144 YPSGHTSIGMATLVLAELNFORONEILKRGYLEGSRVICYGHWSVDPAARIYGSAAV 203
DB 163 YPSGHTTIGMSVALILAEILIPDPAANILORGOIFGTSRIYCGAHWFSVDQAGYIMASGEI 222
QY 204 ATLHTNPAFOOOLQAKOEFAKTO 227
DB 223 AALHGADFRDMELARKLELEKAR 246

RESULT 6

E87293
acid phosphatase [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 25-Aug-2003
C/Accession: E87293
R.Nierman, M.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DebRoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: E87293
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-258 <STO>
A/Cross-references: GB:AE005673; NID:g13421511; PIDN:AAK22345.1; GSPDB:GN00148
A/Genetics:
A/Experimental source: strain PA0190
C/Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

Query Match 23.4%; Score 274.5; DB 2; Length 258;
Best Local Similarity 36.3%; Pred. No. 2.2e-16;
Matches 77; Conservative 31; Mismatches 97; Indels 7; Gaps 7;
QY 12 PDLVYLKNAQATDSLLALPPPEVSGIAFLNDQAMYEKGRLLRNTBGRKLAEDANLSAG 71
DB 25 PSNRRLANG-VFDADHLPPEPAKSEALRDRERIFRATRLAKDTPRMSLAGE-NVEE- 81
QY 72 GVANAFSSAFG-SPITTEKADPOLHKLITNMIEDAGDLATRSAREKYMIRPPAFYGVSTC 130
DB 82 KVLDDYACALGVTPSPFERR-PKLAATYILRMSRDVS-AVAGPKLTKRRRPFSESGPLC 139
QY 131 NITEODKLSKNGSYSGHTSIGMATLVLAELNFORONEILKRGYLEGSRVICYGHWS 190
DB 140 -IKRSLGLALSPDYSGHATWMSVGLVLAEPDRREAILARAQYGGSRVVCVHNMS 198
QY 191 DYDARIVGSAAVATLHTNPAFOOOLQAKDE 222
DB 199 SVEAGRMNAENILSALKSSDAFKADLAARAE 230

RESULT 7

T28698
hypothetical protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T28698
R.Parkhill, J.; Bentley, S.D.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1999
A/Reference number: Z20512
A/Accession: T28698
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2314 <PAR>

A/Cross-references: UNIPROT:O69822; EMBL:AL023496; NID:e1292348; PID:e1292365; PIDN:CAAL
Query Match 15.9%; Score 186; DB 2; Length 2314;
Best Local Similarity 31.0%; Pred. No. 2.1e-07;
Matches 53; Conservative 26; Mismatches 78; Indels 14; Gaps 5;

QY 62 AAEDANLS-AGGVANAFSSAFGSPTTEKADPOLHKLITNMIE--DAGDLATRSAREKYMIR 118
DB 1878 ASNSATVTMMADGSLRGLPLVGEALKEGRLLKTSALFRVENVENDTHD-----AAKNHGY 1933
QY 119 IRPF---APYGVSTCNTTEODK---LSKNGSYSGHTSIGMATLVLAELNFORONEIL 171
DB 1934 LRPIYRLGAFGIDGGAIVESQDSYSGLAGOSYSPSGHTYGGVEAGTIATLLPDLAPSL 1993
QY 172 KRGYLEGSRVICYGHWSVDPAARIYGSAAVATLHTNPAFOOOLQAKDE 222
DB 1994 ARTSEYGDNRIVLGFHYPLDVWGGRITQATVAAHRMADPEPAKLGQAHT 2044

RESULT 8

C63621
Probable acid phosphatase PA0190 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 25-Aug-2003
C/Accession: C63621
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lapidis, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C63621
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-241 <STO>
A/Cross-references: GB:AE004457; GB:AE004091; NID:g9946024; PIDN:AAG03580.1; GSPDB:GN001
A/Experimental source: strain PA01
A/Genetics:
A/Status: preliminary
C/Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do

Query Match 13.7%; Score 161; DB 2; Length 241;
Best Local Similarity 26.5%; Pred. No. 1.5e-06;
Matches 54; Conservative 36; Mismatches 88; Indels 26; Gaps 7;
QY 29 LPPEVSGIAFLNDQAMYEKGRLLRNTBGRKLAEDANLSAGGVANAFSSAFG 82
DB 43 LPPEPADSAALVADLGAVALRQLRTPRQVRRVADNDQMEDNVFPFAGDILGASFDRER 102
QY 83 SPITTEKADPOLHKLITNMIEDAGDLATRSAREKYMIRPPAFYGVSTCNTTEODK---L 138
DB 103 LPLTRS---FNRQENIVE-----VLMPAKHFARPRPY-----EVPRKVRVLP 146
QY 139 SKNGSYSGHTSIGMATLVLAELNFORONEILKRGYLEGSRVICYGHWSVDPAARIV 198
DB 147 PEGSYSGHTTMDSYFKAASLSMLVPEHNDAPFAAEHNASRVLGAGNHFSDLEGQTA 206
QY 199 GSAAVATLHTNPAFOOOLQAKDE 222
DB 207 AALVAVSLADPAVAADPAVAREE 230

RESULT 9

C63691
uncharacterized protein, containing probable phosphatase domain [imported] - Clostridium
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: C63691
R.Nolling, U.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: C96991
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-591 <KUR>
A/Cross-references: UNIPROT:Q97124; GB:AE001437; PIDN:AAK78718.1; PID:g15023624; GSPDB:C
A/Experimental source: Clostridium acetobutylicum ATCC624
C/Genetics:
A/Gene: CAC0742

Query Match 12.9%; Score 151; DB 2; Length 591;
Best Local Similarity 27.2%; Pred. No. 3.8e-05;
Matches 55; Conservative 27; Mismatches 72; Indels 48; Gaps 8;

QY 39 AFINDQAMYEKGRLLRTERGKLA---EDANISAGVNAFSSAGSPITE---KDAI 91
DB 113 AYLDNR-----RNGNYSVLDGLGPKDAFKAGCA-----GTTTVDVTPDAI 155
QY 92 QLN-----KLTNMTEDAGDI-----ATRSKEXKMRIRPFAYG-VSTC 130
DB 156 NVOYTDKGNMAGNNAEESDLSGVKLVDTIRNSAATTPAKOVYKYPFRWRMSDKVKL 215
QY 131 NTEBQDL---SKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYH 187
DB 216 PTLVPEKSTNPPSSGCGFSGHTNATTDALALAVAVERYQEWLTRASLGNDRIVAGMH 275
QY 188 WQSDVDARIIVGSAVVAATLHTN 209
DB 276 SPLDVIGRWATPAIAASALNN 297

RESULT 10

AB3118
serine protease Atu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AB3118
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavhin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; M0ID:21608550; PMID:11743193
A/Accession: AB3118
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-660 <KUR>
A/Cross-references: UNIPROT:Q8U788; GB:AE008689; PIDN:AAU45360.1; PID:g17743054; GSPDB:C
A/Experimental source: strain C58 (dupont)
C/Genetics:
A/Gene: Atu4566
A/Map position: linear chromosome

Query Match 12.5%; Score 147; DB 2; Length 660;
Best Local Similarity 36.3%; Pred. No. 9.7e-05;
Matches 33; Conservative 17; Mismatches 37; Indels 4; Gaps 1;

QY 139 SKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYHOSDVAARIY 198
DB 288 AKDGGFPGHTNAAVLAIAVAVPERFSELTASAELGSRIVAGMHSPLDVIGRIT 347
QY 199 GSAVVAATLHTNPAFQOLOKAKDE---FAK 225
DB 348 ATMAAAMLODPKNAEVKKAHDAVEAYFAK 378

RESULT 11

E98169
serine protease XF0267 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: E98169

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A/Reference number: A97359; M0ID:21608551; PMID:11743194
A/Accession: E98169
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-660 <KUR>
A/Cross-references: UNIPROT:Q8U788; GB:AE007870; PIDN:AAK88879.1; PID:g15158646; GSPDB:C
C/Genetics:
A/Gene: AGR_L_612
A/Map position: linear chromosome

Query Match 12.5%; Score 147; DB 2; Length 660;
Best Local Similarity 36.3%; Pred. No. 9.7e-05;
Matches 33; Conservative 17; Mismatches 37; Indels 4; Gaps 1;

QY 139 SKNGSYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYHOSDVAARIY 198
DB 288 AKDGGFPGHTNAAVLAIAVAVPERFSELTASAELGSRIVAGMHSPLDVIGRIT 347
QY 199 GSAVVAATLHTNPAFQOLOKAKDE---FAK 225
DB 348 ATMAAAMLODPKNAEVKKAHDAVEAYFAK 378

RESULT 12

F75447
vanadium chloroperoxidase-related protein - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: F75447
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R.D.; Dodson, R.J.; i
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; M0ID:2003896; PMID:10567266
A/Accession: F75447
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-145 <WHI>
A/Cross-references: UNIPROT:Q9BV13; GB:AE001953; GB:AE000513; NID:96458740; PIDN:AAF10585
A/Experimental source: strain R1
C/Genetics:
A/Gene: DR1014
A/Map position: 1

Query Match 9.0%; Score 105; DB 2; Length 145;
Best Local Similarity 37.5%; Pred. No. 0.0577;
Matches 24; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 143 SYPSGHTSIGMATLVLAELINPQRONEILKRGYELGESRVICGYHOSDVAARIYSAV 202
DB 77 SYPSGHATVSGAAAEVLAQFFLQARQLRRDARDAFSSVVGIIHMGVDVAGLDVGQRY 136
QY 203 VATL 206
DB 137 ARAL 140

RESULT 13

A87623
PAP2 homolog protein [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: A87623
R/Nierman, W.C.; Feibjyrum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolm
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87623
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <STO>
A:Cross-references: UNIPROT:Q9A424; GB:AE005673; NID:g13424659; PIDN:AAK24981.1; GSPDB:G
C:Genetics: CC3019
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 8.4%; Score 98.5; DB 2; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.46;
Matches 34; Conservative 13; Mismatches 42; Indels 19; Gaps 3;

QY 104 AGDLATRAKEKYMIRPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVL----- 159
DB 136 SGVTVSQSLKAVGERDEAYRVE-----AVNASFSPSGHAMSAVFLTLGVLA 186

QY 160 AEINPQRONEILKRGYE-----LGESRYICGYHMQSDVDAAIRIVGSA 201
DB 187 ARFSRRKVKILAVSAVVVSLVCGASRYLGVHVSVDVLGMSVGAA 234

RESULT 14
D82070
conserved hypothetical protein VC2488 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82070
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <HEI>
A:Cross-references: UNIPROT:Q9K985; GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAFP563
C:Genetics:
A:Experimental source: serogroup O1, strain N16961; biotype El Tor
A:Gene: VC2488
A:Map position: 1
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 8.2%; Score 96; DB 2; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.45;
Matches 27; Conservative 13; Mismatches 43; Indels 4; Gaps 1;

QY 113 KEKWRIRPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVLAENPQRONEILK 172
DB 81 KNSFQRRRPOELSAVLTAYITPSDRY---SLPSGHTAAAFMATLIGIYFHWYAVALC 136

QY 173 RGYELGESRVICGYHMQSDVDAAIRIVG 199
DB 137 WAGLIGLARVLGVHFLSDVITAGALLG 163

RESULT 15
T07064
seed biotin-containing protein LEA [validated] - soybean
C:Species: Glycine max (soybean)
C:Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 09-Jul-2004
C:Accession: T07064
R:Hsing, Y.C.; Tsou, C.H.; Hsu, T.F.; Chen, Z.Y.; Hsieh, K.L.; Hsieh, J.S.; Chow, T.Y.
A:Title: Tissue- and stage-specific expression of a soybean (Glycine max L.) seed-mature
A:Reference number: Z15895; MUID:98418627; PMID:9747855
A:Accession: T07064
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-643 <HSI>

A:Cross-references: UNIPROT:Q39846; EMBL:U59626; NID:g1389896; PIDN:AA61783.1; PID:g138;
A:Experimental source: strain Shi-shi; cotyledon
C:Superfamily: pea seed biotin-containing protein
C:Keywords: biotin binding; seed
F:125/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 8.0%; Score 93.5; DB 1; Length 643;
Best Local Similarity 27.5%; Pred. No. 4.2;
Matches 50; Conservative 20; Mismatches 73; Indels 39; Gaps 9;

QY 44 QAMTEKGRLLNTERGKLAEDANLSAGVANAFSAFG--SPITEKD-APQLHKILTN 99
DB 165 QVVAEKGR-ETETARGVGAENEGARTTAVITCTLEKGGTQKPIREBERESERSAME 223

QY 100 MIEDAGDLATRSAREKYMIRPPAFYGVSTCNTTEODKLSKNGSYPSGHTSIGMATLVL 159
DB 224 QISVSDQATGVGKEXERAKQAA--SETINTTTQTRQES-----AQAKNL 268

QY 160 AEINPQRONEILKRGYEIGESRVICGYHMQSDVDAAIRIVGSAVVATLHTNPAPFOOQLQKA 219
DB 269 A---AQAKDALTLEKQQ-----GVAVTYDT-----ISSAAKTAASEKTALV---AEKA 309

QY 220 KD 221
DB 310 KD 311

Search completed: March 2, 2005, 20:27:46
Job time : 26.3333 secs

This Page Blank (uspio)